

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:18:13 ; Search time 20.3912 Seconds  
(without alignments)  
2367.669 Million cell updates/sec

Title: US-09-783-931-2  
Perfect score: 4153  
Sequence: 1 MGRFLTLALLSALLCRCQ.....YQSVVISEKDECIATEV 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4153	100.0	728	3	US-08-981-392-2
2	4153	100.0	728	4	US-09-908-322-2
3	4142.5	99.7	729	3	US-08-872-855-8
4	3495.5	84.2	721	3	US-08-981-392-5
5	3495.5	84.2	721	4	US-09-908-322-5
6	3494.5	84.1	723	3	US-09-068-740A-9
7	3494.5	84.1	723	4	US-09-423-753-27
8	3494.5	84.1	723	4	US-10-140-002-346
9	3491.5	84.1	721	3	US-08-872-855-7
10	3466.5	83.5	723	4	US-09-641-612-6
11	3445.5	83.0	702	3	US-09-068-740A-4
12	3375	81.3	720	3	US-08-872-855-4
13	3368	81.1	722	3	US-08-981-392-12
14	3368	81.1	722	4	US-09-908-322-12
15	3346.5	80.6	713	3	US-08-872-855-5
16	3061.5	73.7	717	3	US-08-872-855-9
17	2784	67.0	520	3	US-09-068-740A-3
18	2489	59.9	578	3	US-08-981-392-13
19	2489	59.9	578	4	US-09-908-322-13
20	1928	46.4	642	3	US-08-872-855-10
21	1897	45.7	685	3	US-08-872-855-2
22	1897	45.7	685	4	US-09-423-753-25
23	1897	45.7	685	4	US-09-641-612-7
24	1897	45.7	685	4	US-10-140-002-88
25	1887	45.4	659	4	US-09-423-753-3
26	1693.5	40.8	500	4	US-09-423-753-2
27	1559.5	37.6	833	1	US-08-264-534-6

28	1559.5	37.6	833	1	US-08-083-590A-2	Sequence 2, Appli
29	1559.5	37.6	833	1	US-08-465-500-6	Sequence 6, Appli
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31	1559.5	37.6	833	2	US-08-346-128-6	Sequence 6, Appli
32	1559.5	37.6	833	3	US-08-532-384-2	Sequence 2, Appli
33	1559.5	37.6	833	3	US-08-893-828-6	Sequence 6, Appli
34	1555.5	37.5	832	3	US-08-981-392-6	Sequence 6, Appli
35	1555.5	37.5	832	4	US-09-908-322-6	Sequence 6, Appli
36	1534.5	36.9	830	3	US-08-872-855-11	Sequence 11, Appl
37	1354	32.6	1218	2	US-08-400-159-6	Sequence 6, Appli
38	1354	32.6	1218	3	US-08-611-729A-6	Sequence 6, Appli
39	1354	32.6	1218	4	US-09-917-254-85	Sequence 85, Appl
40	1354	32.6	1218	4	US-09-195-524-6	Sequence 6, Appli
41	1353	32.6	1208	4	US-09-199-865-1	Sequence 1, Appli
42	1349	32.5	1219	3	US-08-882-046-5	Sequence 5, Appli
43	1349	32.5	1219	4	US-09-566-047-5	Sequence 5, Appli
44	1348.5	32.5	1193	2	US-08-400-159-10	Sequence 10, Appl
45	1348.5	32.5	1193	3	US-08-611-729A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-08-981-392-2  
; Sequence 2, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 728 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-981-392-2

Query Match 100.0%; Score 4153; DB 3; Length 728;  
Best Local Similarity 100.0%; Pred. No. 1.1e-304;  
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 601 LANCQREKDISISVIGATQIKNTNKKVDVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEEDSV 660  
D 601 LANCQREKDISISVIGATQIKNTNKKVDVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEEDSV 660  
QY 661 KEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKD 720  
D 661 KEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKD 720  
QY 721 ECIIATEV 728  
D 721 ECIIATEV 728

RESULT 3  
US-08-872-855-8  
; Sequence 8, Application US/08872855  
; Patent No. 6121045  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND  
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,855  
; FILING DATE: 11-JUN-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MAA-003.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-855-8

Query Match 99.7%; Score 4142.5; DB 3; Length 729;  
Best Local Similarity 99.9%; Pred. NO. 6.5e-304;  
Matches 728; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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D 1 MGRFLLTLALLSALLCQVDGSGVFELKLOBFVNKGLLSNRNCCRGPGGAGQQQC 60  
QY 61 DCKTFFRVCLKHQASVSPPECTYGSAITPVLGANSFSVPDGGAGADPAFSPNIRFPFG 120  
D 61 DCKTFFRVCLKHQASVSPPECTYGSAITPVLGANSFSVPDGGAGADPAFSPNIRFPFG 120  
QY 121 FTWPGTFSLLIEALHTDSPDDLTATENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 180  
D 121 FTWPGTFSLLIEALHTDSPDDLTATENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 180  
QY 181 SYRFVCDHYHYEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQ 240

08/832,633  
4/4/97

Db 181 SYRFVCDHYHYEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQ 240  
QY 241 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCT 300  
D 241 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCT 300  
QY 301 HHKPKNGATCTNTGQGSYTCSCRPGYTGSSCEIIEINECNANPCNKGSGSCTDLNYSYCT 360  
D 301 HHKPKNGATCTNTGQGSYTCSCRPGYTGSSCEIIEINECNANPCNKGSGSCTDLNYSYCT 360  
QY 361 CPPGFYGNKNCSELSAMTCAAGPCFNGGRCRTPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420  
D 361 CPPGFYGNKNCSELSAMTCAAGPCFNGGRCRTPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420  
QY 421 CANGAQ-CVDLGNYSYICQCAAGTGRHCDNVDVDDCASFPVNGGTCQDGVNDYSCTCPPG 479  
D 421 CANGAQACVDLGNYSYICQCAAGTGRHCDNVDVDDCASFPVNGGTCQDGVNDYSCTCPPG 480  
QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHEHNSRNYVCECARGYGLNCQFLLPEPQGPVIVDF 539  
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QY 540 TEKYTEGONSQFPWIAVCAGIILVLMLLGCAAIWCVRLKVQKRHHQPEACRSETETMN 599  
D 541 TEKYTEGONSQFPWIAVCAGIILVLMLLGCAAIWCVRLKVQKRHHQPEACRSETETMN 600  
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QY 660 VKEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEK 719  
D 661 VKEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEK 720  
QY 720 DECIIATEV 728  
D 721 DECIIATEV 729

RESULT 4  
US-08-981-392-5  
; Sequence 5, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-981-392-5

Query Match      84.2%; Score 3495.5; DB 3; Length 721;
Best Local Similarity 82.2%; Pred. No. 3.7e-255;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCCRGGPGG-AGQQQ 59
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Qy 60 CDCKTFFRVCLKHYSQASVSPPEPCTYGSAITPVLGANSFSPVDGAGGADPAFSPNIRPFP 119
Db 56 CECKTFFRICLKHYSQSNVSPPEPCTYGGAVTPVLGNTSNFVVPE-SSNADPTFSNIRPFP 114

Qy 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEESQDLHSSGRTDLK 179
Db 115 GFTWPGTFSLLIEAIIHADSDADDLNTENPERLISRLATORHLTVGEQWSQDLHSSDRTELK 174

Qy 180 YSYRFVCDHEYHYGEGSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDE 239
Db 175 YSYRFVCDHEYHYGEGCSDYCRPRDDAFGHFSCGEKGLCNPGWKGLYCTEPICLPGCDE 234

Qy 240 QHGFCDKPGECKRCRVGWQGRYDCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYC 299
Db 235 HHGYCDKPGECKRCRVGWQGRYDCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYC 294

Qy 300 THHKPCKNKGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDLENSYSC 359
Db 295 THHKPCENGATCTNTGQGSYTCSCRPGYTGSGNCEIEVNECDANPCKNGGSCDLENSYTC 354

Qy 360 TCPGPFYKNCELSAMTCADGCFNGGRCTDNDPGGYSRCPLGYSGFNCEKKIDYCSSS 419
Db 355 SCPPGFYKNCELSAMTCADGCFNGGRCADNPDGGYICFCPVGYSGFNCEKKIDYCSSN 414

Qy 420 PCANGAQCVDLGNYSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCCQDGVNDYSCTCPPG 479
Db 415 PCANGARCEDLGNYSYICQCQEGFSGRNCDNLDCTSFPCQNGGTCCQDGINYSCTCPPG 474

Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
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Qy 600 NLANCQREKDISISVIGATOIKNTNKKVDFHSD-NSDKNGYKVRYPSPVDYNLVHELKNE 658
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Qy 659 SVKEHKGCEAKCETYDSEAEKSQVQLKSSDTSERKRDPSPVYSTSKDTKYQSVYVISEE 718
Db 653 SPKERSKCEAKCSSNDSSEDVNSVHSK-RDSSERRRDPDSAYSTSKDTKYQSVYVISDE 711

Qy 719 KDECIATEV 728
Db 712 KDECIATEV 721

RESULT 5
US-09-908-322-5
; Sequence 5, Application US/09908322
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; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
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Query Match      84.2%; Score 3495.5; DB 4; Length 721;
Best Local Similarity 82.2%; Pred. No. 3.7e-255;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCCRGGPGG-AGQQQ 59
Db 1 MGQORMLTLVL SAVL--CQISCSGLFELRLQEFVNKKGLLGNNMCCR---PGSLASLQR 55

Qy 60 CDCKTFFRVCLKHYSQASVSPPEPCTYGSAITPVLGANSFSPVDGAGGADPAFSPNIRPFP 119
Db 56 CECKTFFRICLKHYSQSNVSPPEPCTYGGAVTPVLGNTSNFVVPE-SSNADPTFSNIRPFP 114

Qy 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEESQDLHSSGRTDLK 179
Db 115 GFTWPGTFSLLIEAIIHADSDADDLNTENPERLISRLATORHLTVGEQWSQDLHSSDRTELK 174

Qy 180 YSYRFVCDHEYHYGEGSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDE 239
Db 175 YSYRFVCDHEYHYGEGCSDYCRPRDDAFGHFSCGEKGLCNPGWKGLYCTEPICLPGCDE 234

Qy 240 QHGFCDKPGECKRCRVGWQGRYDCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYC 299
Db 235 HHGYCDKPGECKRCRVGWQGRYDCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYC 294

Qy 300 THHKPCKNKGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDLENSYSC 359
Db 295 THHKPCENGATCTNTGQGSYTCSCRPGYTGSGNCEIEVNECDANPCKNGGSCDLENSYTC 354
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Db 295 THHKPCENGATCTNTGQSYTCSRPGYTGSGNCEIEVNECDANPCNKGSGCSDLNSYTC 354  
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Db 355 SCPPGFYGNKCELSAMTADGPCFNGGRCADNPDDGGYICFCVPYSGFNCCKIDYCSSN 414  
QY 420 PCANGAQCVDLGNSYICQCAQFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479  
Db 415 PCANGARCEDLNSYICQCEGFSGRNCDNDLDDCTSPPCQNGGTCQDGINYSCTCPPG 474  
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QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAVVVCVRLKVQKRHHQPEACRSETETMN 599  
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QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNE 658  
Db 593 NLANCQREKDISVSFIGTQIKNTNKKIDFLSENNKNGYKPRYPSVDYNLVHELKNE 652  
QY 659 SVKEEHGKCEAKCETYDSEABEKSAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVYVISEE 718  
Db 653 SPKEERSKCEAKCSSNDSSEVDNSVHSK-RDSSERRRPPDSAYSTSKDTKYQSVYVISDE 711  
QY 719 KDECIATEV 728  
Db 712 KDECIATEV 721

RESULT 6  
US-09-068-740A-9  
; Sequence 9, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-9

Query Match 84.1%; Score 3494.5; DB 3; Length 723;  
Best Local Similarity 83.3%; Pred. No. 4.4e-255;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;  
QY 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQWSSGSGVFELKLOEFVNKKGLLGNRNCCR---GGAGPPPC 54  
QY 61 DCKTFFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSVPDAGGADPAFSPNPIRFPFG 120  
Db 55 ACRTFFRVCLKHQASVSPPEPCTYGSATVPVLGVDSFSLPDG--GGADSAFSPNPIRFPFG 113  
QY 121 FTWPGTFSLLIEALHTDSPDDLTTHENPERLISRLATQRLHVLAVGEWSQDLHSSGRTDLKY 180  
Db 114 FTWPGTFSLLIEALHTDSPDDLATENPERLISRLATQRLHVLTVGEWSQDLHSSGRTDLKY 173  
QY 181 SYRFVCDHYHGECSVFCRPRDRDFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQ 240

Db 174 SYRFVCDHYHGECSVFCRPRDDAFGHFTCGERGEKVCNPGWKPYCTEPICLPGCDEQ 233  
QY 241 HGFCDKPGECKCRVGMQGRYCDDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 300  
Db 234 HGFCDKPGECKCRVGMQGRYCDDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 293  
QY 301 HHKPCNGATCTNTGQSYTCSRPGYTGSGSCEIEINECDANPCNKGSGCSDLNSYSCT 360  
Db 294 HHKPCNGATCTNTGQSYTCSRPGYTGATCBLGIDECDDPSCKNGSGCSDLNSYSCT 353  
QY 361 CPPGFYGNKCELSAMTADGPCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSP 420  
Db 354 CPPGFYGNKCELSAMTADGPCFNGGRCSDSPDGGYSCRCVPYSGFNCCKIDYCSSSP 413  
QY 421 CANGAQCVDLGNSYICQCAQFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGY 473  
QY 481 NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGNPCQFLLPELPGPAVVDLT 533  
QY 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAVVVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGPFPWAVACAGVILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN 592  
QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNE 658  
Db 593 LANCQREKDISVSIIGATQIKNTNKKADFGHDSADKNGFKARYPAVDYNLVQDLKGDDT 652  
QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVYVISE 717  
Db 653 AVRDAHSKRDTKCPQPGSSGEEKGTPTTLRGGEASERKRPDSCGSTSKDTKYQSVYVISE 712  
QY 718 EKDECIATEV 728  
Db 713 EKDECIATEV 723

RESULT 7  
US-09-423-753-27  
; Sequence 27, Application US/09423753  
; Patent No. 6664098  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR  
; FILE REFERENCE: KP-8693  
; CURRENT APPLICATION NUMBER: US/09/423,753  
; CURRENT FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: PCT/JP98/02104  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 9/124064  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-753-27

Query Match 84.1%; Score 3494.5; DB 4; Length 723;  
Best Local Similarity 83.3%; Pred. No. 4.4e-255;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;  
QY 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQWSSGSGVFELKLOEFVNKKGLLGNRNCCR---GGAGPPPC 54  
QY 61 DCKTFFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSVPDAGGADPAFSPNPIRFPFG 120  
Db 55 ACRTFFRVCLKHQASVSPPEPCTYGSATVPVLGVDSFSLPDG--GGADSAFSPNPIRFPFG 113

Qy 121 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKY 180  
Dbb 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATORHLTVGEEWSQDLHSSGRTDLKY 173  
Qy 181 SYRFVCDHEHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
Dbb 174 SYRFVCDHEHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233  
Qy 241 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300  
Dbb 234 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 293  
Qy 301 HHKPCKNKGATCTNTGQSGYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDTDLNYSCT 360  
Dbb 294 HHKPCKNKGATCTNTGQSGYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTDLNYSCT 353  
Qy 361 CPPGFYGNKCELSAMTCADGPGCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSP 420  
Dbb 354 CPPGFYGNKCELSAMTCADGPGCFNGGRCSDSPDDGGYSCRCPCVGYSGFNCCKIDYCSSSP 413  
Qy 421 CANGAQCVDLGNYSYICQCAQAGTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Dbb 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPCANGGTCRDGVNDFSCTCPGGY 473  
Qy 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPQGPVIVDFT 540  
Dbb 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAVVVCVRLKVQKRHHQPEACRSETETMNN 600  
Dbb 534 EK-LEGQGGPFPWAVACAGVILVLMLLLGCAAVVVCVRLRLQKRPADPCRGETETMNN 592  
Qy 601 LANCQREKDISISVIGATQIKNTNKKVDHFSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658  
Dbb 593 LANCQREKDISVSIIGATQIKNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDT 652  
Qy 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Dbb 653 AVRDAHSKRDTKCPQPGSSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712  
Qy 718 EKDECIIATEV 728  
Dbb 713 EKDECVIATEV 723

RESULT 8  
US-10-140-002-346  
; Sequence 346, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-002-346

Query Match 84.1%; Score 3494.5; DB 4; Length 723;  
Best Local Similarity 83.3%; Pred. No. 4.4e-255;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNNKGLLSNRNCCRGGGPGGAGQQQC 60  
Dbb 1 MGSRCALALAVLSALL--CQWSSGVFELKQEFVNNKGLLGNRNCCR---GGAGPPPC 54  
Qy 61 DCKTFFRVCLKHYQASVSPPEPCTYGSAITPVLGANSFSVPDAGGADPAFSNPIRFPFG 120  
Dbb 55 ACRTFFRVCLKHYQASVSPPEPCTYGSAVTPVLGVDSFSLPDG-GGADSAFSNPIRFPFG 113  
Qy 121 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKY 180  
Dbb 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATORHLTVGEEWSQDLHSSGRTDLKY 173  
Qy 181 SYRFVCDHEHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
Dbb 174 SYRFVCDHEHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233  
Qy 241 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300  
Dbb 234 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 293  
Qy 301 HHKPCKNKGATCTNTGQSGYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDTDLNYSCT 360  
Dbb 294 HHKPCKNKGATCTNTGQSGYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTDLNYSCT 353  
Qy 361 CPPGFYGNKCELSAMTCADGPGCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSP 420  
Dbb 354 CPPGFYGNKCELSAMTCADGPGCFNGGRCSDSPDDGGYSCRCPCVGYSGFNCCKIDYCSSSP 413  
Qy 421 CANGAQCVDLGNYSYICQCAQAGTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Dbb 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPCANGGTCRDGVNDFSCTCPGGY 473  
Qy 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPQGPVIVDFT 540  
Dbb 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAVVVCVRLKVQKRHHQPEACRSETETMNN 600  
Dbb 534 EK-LEGQGGPFPWAVACAGVILVLMLLLGCAAVVVCVRLRLQKRPADPCRGETETMNN 592  
Qy 601 LANCQREKDISISVIGATQIKNTNKKVDHFSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658  
Dbb 593 LANCQREKDISVSIIGATQIKNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDT 652  
Qy 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Dbb 653 AVRDAHSKRDTKCPQPGSSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712  
Qy 718 EKDECIIATEV 728  
Dbb 713 EKDECVIATEV 723

RESULT 9  
US-08-872-855-7  
; Sequence 7, Application US/08872855  
; Patent No. 6121045  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND

; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-7

Query Match 84.1%; Score 3491.5; DB 3; Length 721;
Best Local Similarity 82.1%; Pred. No. 7.4e-255;
Matches 599; Conservative 65; Mismatches 55; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGPGG-AGQQQ 59
Dd 1 MGQRMJTLVLAVL--CQISCSGLFELRLQEFVNKKGLLGNNMCCR--PGSLASLQR 55

QY 60 CDCKTFRVCLKHQYQASVSPPEPCTYGSATIPVLGANSFVSVPDGGAGDPAFSPNIRFPF 119
Dd 56 CECKTFRICLKHQYQASVSPPEPCTYGGAVTPVLGTFNSFWPE-SSNADPTFSNIRFPF 114

QY 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHLAGVEEWSQDLHSSGRTDLK 179
Dd 115 GFTWPGTFSLLIEALHADSADDLNTENPERLISRATQRLHLAGVEEWSQDLHSSDRTDLK 174

QY 180 YSRFVCDHEYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDE 239
Dd 175 YSRFVCDHEYHYGEGCSVFCRPRDDAFGHFSCGEGKGENLCNPGWKGLYCTEPICLPGCDE 234

QY 240 QHGFCDKPGECKRCRVGWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYC 299
Dd 235 HHGYCDKPGECKRCRVGWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYC 294

QY 300 THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNKGSCDTLENSYSC 359
Dd 295 THHKPCENGATCTNTGQGSYTCSCRPGYTGSNCEIEWNECDANPCKNKGSCDTLENSYTC 354

QY 360 TCPPGFYGNKCELSAMTCADGPGCFNGGRCITDNPBGYSRCRPLGYSYGFNCEKKIDYCSSS 419
Dd 355 SCPPGFYGNKCELSAMTCADGPGCFNGGRCADNPBGYICPCPVGYSYGFNCEKKIDYCSSN 414

QY 420 PCANGAQCVDLGNYSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPG 479
Dd 415 PCANGARCEDLGNYSYICQCEGFGSRNCDNDLDDCTSFPCQNGGTCQDGVNDYSCTCPPG 474

QY 480 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPQGPVIVDF 539
Dd 475 YIGKNCMPITKCEHNPCHNGATCHERNRYYVQCARGYGGNNCQFLLPE--EKPVVVDL 532

QY 540 TEKYTEGONSQFPWIAVCAGIILVLMLLIGCAAIVVCVRLKVQKRHHQPEACRSETETMN 599
Dd 533 TEKYTEGQSQGFPWIAVCAGIVLVLMLLIGCAAIVVCVRLKVQKRHHQPEACRSETETMN 592
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRYPVDYNLVHELKNE 658
Dd 593 NLANCQREKDISVSFIGTTQIKNTNKKIDFLSENNEKNGYKPRYPVDYNLVHELKNE 652
QY 659 SVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVYVISEE 718
Dd 653 SPKEERSKCEAKCSSNDSDESVNSVHSK-RDSSERRRRPDSAYSTSKDTKYQSVVVISDE 711
QY 719 KDECIITAEV 728
Dd 712 KDECIITAEV 721

RESULT 10
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match 83.5%; Score 3466.5; DB 4; Length 723;
Best Local Similarity 82.8%; Pred. No. 5.7e-253;
Matches 605; Conservative 47; Mismatches 68; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60
Dd 1 MGSRCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLGNNMCCR---GGAGPPPC 54

QY 61 DKCTFRVCLKHQYQASVSPPEPCTYGSATIPVLGANSFVSVPDGGAGDPAFSPNIRFPFG 120
Dd 55 ACRTFRVCLKHQYQASVSPPEPCTYGSATIPVLGVDVSFSLPDG-GGADSAFSPNIRFPFG 113

QY 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRLHLAGVEEWSQDLHSSGRTDLKY 180
Dd 114 FTWPGTFSLLIEALHTDSPDDLATENPERLISRATQRLHLAGVEEWSQDLHSSGRTDLKY 173

QY 181 YSRFVCDHEYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Dd 174 YSRFVCDHEYHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGECKRCRVGWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCT 300
Dd 234 HGFCDKPGECKRCRVGWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCT 293

QY 301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNKGSCDTLENSYSCT 360
Dd 294 HHKPCKNGATCTNTGQGSYTCSCRPGYTGATCELIGIDECDPSPCKNKGSCDTLENSYSCT 353

QY 361 CPPGFYGNKCELSAMTCADGPGCFNGGRCITDNPBGYSRCRPLGYSYGFNCEKKIDYCSSSP 420
Dd 354 CPPGFYGNKCELSAMTCADGPGCFNGGRCSDSPDGGYSRCRCPVGYSGFNCEKKIDYCSSSP 413

QY 421 CANGAQCVDLGNYSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480
Dd 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPPGY 473

QY 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPQGPVIVDFT 540



Db 474 TGRNCAPVSRCEHAPCHNGATCHERGHYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
Qy 541 EKYTEQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGPFPWAVAVCAGVILVLMLLGCAAVVVCVPLRLQKHRPPADPCRGETETMNN 592  
Qy 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSPVDYNLVHELKNE- 658  
Db 593 LANCOREKDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDT 652  
Qy 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVVYISE 717  
Db 653 AVRDAHSKRDTKCQPOGSSGEEKGTPPTTLRGGEASERKRDPDSGCSTSKDTKYQSVVYISE 712  
Qy 718 EKDECIIATEV 728  
Db 713 EKDECVIATEV 723

RESULT 11  
US-09-068-740A-4  
; Sequence 4, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 702  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-4

Query Match 83.0%; Score 3445.5; DB 3; Length 702;  
Best Local Similarity 84.0%; Pred. No. 2.1e-251;  
Matches 595; Conservative 46; Mismatches 58; Indels 9; Gaps 6;  
Qy 24 SGVFELKLOEFVNKGLLSNRNCCRGGPGGAGQQQCDCKTFFRVCLKHQYASVSPEPPC 83  
Db 1 SGVFELKLOEFVNKGLLGNRCR---GGAGPPPCACETFFRVCLKHQYASVSPEPPC 56  
Qy 84 TYGSAITPVLGANSFSVPDGAGADPAFNSPIRFPFGFTWPGTFSLIIEALHTDSPDDL 143  
Db 57 TYGSAVTPVLGVDSFSLPDG-GGADSAFNSPIRFPFGFTWPGTFSLIIEALHTDSPDDLA 115  
Qy 144 TENPERLISRLATORHLAVGEWSQDLHSSGRTDLKYSYRFVCDHEYHYGEGCSVFCRPRD 203  
Db 116 TENPERLISRLATORHLTVGEWSQDLHSSGRTDLKYSYRFVCDHEYHYGEGCSVFCRPRD 175  
Qy 204 DRFGHTCGERGEKVCNPGWKGYCTEPICLPGCDEQHGFCDKPGECKCRVWQGRYCDE 263  
Db 176 DAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQHGFCDKPGECKCRVWQGRYCDE 235  
Qy 264 CIRYPGCLHGTCQOPWQCNQCEGWGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCSC 323  
Db 236 CIRYPGCLHGTCQOPWQCNQCEGWGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCSC 295  
Qy 324 RPYGTSSCEIEINECDANPCXNGGSCDTDLSENSYSTCPCPGFYGNCELSAMTCADGPCF 383  
Db 296 RPYGTATGATCELGIDECDPSPCKXNGGSCDTDLSENSYSTCPCPGFYGKICELSAMTCADGPCF 355

Qy 384 NGRRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSYICQCAQGT 443  
Db 356 NGRCSDSPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCSNGAKCVDLGLDAYLCRCQAGFS 415  
Qy 444 GRHCCDNVDDCASFPVCVNGGTQODGVNDYSCTCPGYNKNCSTPVSRCHEHNPCHNGATC 503  
Db 416 GRHCCDNVDDCASSPCANGGTCRDGVNDFSCTCPGTYGRNCSAPVSRCEHAPCHNGATC 475  
Qy 504 HERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGONSQFPWIAVCAGIILV 563  
Db 476 HERGHRYVCECARGYGGPNCQFLLPELPPGPAVVVDLTK-LEGQGGPFPWAVAVCAGVILV 534  
Qy 564 LMLLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNNLANCQREKDISISVIGATQIKNT 623  
Db 535 LMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNT 594  
Qy 624 NKKVDFHSDNS-DKNGYKVRYPSPVDYNLVHELKNE- SVKEEHGKCEAKCETYDSEAEK 681  
Db 595 NKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPOGSSGEEK 654  
Qy 682 -SAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVVYISEEKDECIIATEV 728  
Db 655 GTPPTTLRGGEASERKRDPDSGCSTSKDTKYQSVVYISEEKDECVIATEV 702

RESULT 12  
US-08-872-855-4  
; Sequence 4, Application US/08872855  
; Patent No. 6121045  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND  
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,855  
; FILING DATE: 11-JUN-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MAA-003.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 720 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-855-4

Query Match 81.3%; Score 3375; DB 3; Length 720;  
Best Local Similarity 79.2%; Pred. No. 4.4e-246;  
Matches 579; Conservative 71; Mismatches 67; Indels 14; Gaps 8;  
Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKGLLSNRNCCRGG-GPGGAGQQQ 59



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Db      1  MGRRSALALAVVSALL--CQWSSGVFELKLOEFVFNKXGLLGNRNCCRGSGP-----P 52
QY      60  CDCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSVPDGGAGDPAFSPNPIRFPF 119
Db      53  CACRTFFRVCLKH-QASVSPPEPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFSPNPIRFPF 110
QY     120  GFTWPGTFSLLIEALHTDSDPDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLK 179
Db     111  GFTWPGTFSLLIEALHTDSDPDLATENPERLISRLTQRH-TVGEWSQDLHSSGRTDLR 169
QY     180  YSYRFVCDHYHYGEGSVFCRPRDDRFHFTCGERGKVCNPGWKQYCTEPICLPGCDE 239
Db     170  YSYRFVCDHYHYGEGSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDD 229
QY     240  QHGFCDKPGECKCRVWQGRYCDERYPGCLHGTCQOPWQCNCQEGWGLFCNQDLNYC 299
Db     230  QHGFCDKPGECKCRVWQGRYCDERYPGCLHGTCQOPWQCNCQEGWGLFCNQDLNYC 289
QY     300  THHKPCKNGATCTNTGQSYTCSRCRPGYTGSSCEIEINECDANPCKNNGSGCTDLENSYSC 359
Db     290  THHKPCRNATCTNTGQSYTCSRCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSC 349
QY     360  TCPPGFYGNKCELSAMTCADGPCFNGGRCRDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419
Db     350  TCPPGFYGNKCELSAMTCADGPCFNGGRCSDNPDGGYTCPCPLGSGFNCEKKMDLCGSS 409
QY     420  PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPVCWGGTCQDGVNDYSCTCPPG 479
Db     410  PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 469
QY     480  YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
Db     470  YTGKNCAPVSRCEHAPCHNGATCHORQRYMCECAQYGGPNCQFLLPEPPGPMVVDL 529
QY     540  TEKYTEGQNSQFPPIAVCAGIILVLMLLGCAAVVVRLLKQKHQHPPEPCGGGETETMN 599
Db     530  SERHMESQGGPFPWVAVCAGVVLVLLLLGCAAVVVRLLKQKHQPPPEPCGGGETETMN 589
QY     600  NLANCQREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLVHELK-NE 657
Db     590  NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAKKSSFVKRYPTVDYNLVRDLKGDE 649
QY     658  DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPSDVYSTSKDTKYQSVYVISE 717
Db     650  ATVRDTHSKRDTKCQSSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSA 709
QY     718  EKDECIIATEV 728
Db     710  EKDECVIATEV 720

RESULT 13
US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; City: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-12

Query Match      81.1%; Score 3368; DB 3; Length 722;
Best Local Similarity 78.5%; Pred. No. 1.5e-245;
Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;

QY      1  MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVFNKXGLLSNRNCCRGG-GPGGAGQQQ 59
Db      1  MGRRSALALAVVSALL--CQWSSGVFELKLOEFVFNKXGLLGNRNCCRGSGP-----P 52
QY     60  CDCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSVPDGGAGDPAFSPNPIRFPF 119
Db     53  CACRTFFRVCLKHQYQASVSPPEPCTYGSATPVLGVDSFSLPDGA-GIDPAFSPNPIRFPF 111
QY     120  GFTWPGTFSLLIEALHTDSDPDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLK 179
Db     112  GFTWPGTFSLLIEALHTDSDPDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLR 171
QY     180  YSYRFVCDHYHYGEGSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDE 239
Db     172  YSYRFVCDHYHYGEGSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDD 231
QY     240  QHGFCDKPGECKCRVWQGRYCDERYPGCLHGTCQOPWQCNCQEGWGLFCNQDLNYC 299
Db     232  QHGFCDKPGECKCRVWQGRYCDERYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYC 291
QY     300  THHKPCKNGATCTNTGQSYTCSRCRPGYTGSSCEIEINECDANPCKNNGSGCTDLENSYSC 359
Db     292  THHKPCRNATCTNTGQSYTCSRCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSC 351
QY     360  TCPPGFYGNKCELSAMTCADGPCFNGGRCRDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419
Db     352  TCPPGFYGNKCELSAMTCADGPCFNGGRCSDNPDGGYTCPCPLGSGFNCEKKMDLCGSS 411
QY     420  PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479
Db     412  PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471
QY     480  YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
Db     472  YTGKNCAPVSRCEHAPCHNGATCHORQRYMCECAQYGGPNCQFLLPEPPGPMVVDL 531
QY     540  TEKYTEGQNSQFPPIAVCAGIILVLMLLGCAAVVVRLLKQKHQHPPEACRSETETMN 599
Db     532  SERHMESQGGPFPWVAVCAGVVLVLLLLGCAAVVVRLLKQKHQPPPEPCGGGETETMN 591
QY     600  NLANCQREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLVHELK-NE 657
Db     592  NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDE 651
QY     658  DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPSDVYSTSKDTKYQSVYVISE 717
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Db 652 ATVRDTHSKRDTKCQSQSLQEKRRSPQHLGVRFLTENRPESVYSTKDTKYQSVYVLSA 711
QY 718 EKDECIATEV 728
Db 712 EKDECVIATEV 722

RESULT 14
US-09-908-322-12
; Sequence 12, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12

Query Match 81.1%; Score 3368; DB 4; Length 722;
Best Local Similarity 78.5%; Pred. No. 1.5e-245;
Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;

QY 1 MGRFLLTALLSALLCRCQVDGSGVFELKQEFVNKKGLLSNRNCCRG-GPGGAGQQQ 59
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Db 1 MGRSALALAVSALL--CQWSSGVFELKQEFVNKKGLGNRNCCRGSGP-----P 52

QY 60 CDCKTFFRVCLKHQASVSPBPCTYGSAITPVLGANSFSPVDGAGGADPAFNSPIRFPF 119
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 CACRTFFRVCLKHQASVSPBPCTYGSATPVLGVDSFSLPDGA-GIDPAFNSPIRFPF 111

QY 120 GFTWPGTFSLIEALHTDSPDLTTENPERLISRATORHLAVGEEWSQDLHSSGRTDLK 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 GFTWPGTFSLIEALHTDSPDLATENPERLISRLTTQRLTVGEEWSQDLHSSGRTDLR 171
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QY 180 YSYRFVCDEHYYGEGCSVFCRPRDRDFGHFTCGERGEKVCNPNWGKQYCTEPICLPGCDE 239
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 172 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKQYCTDPICLPGCCD 231
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 240 QHGFCDKPGECKRVMGQGRYCDICIRYPGCLHGTCCQPWCNCQEGWGGLFCNQDLNYC 299
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 QHGYCDKPGECKRVMGQGRYCDICIRYPGCVHGTCCQPWCNCQEGWGGLFCNQDLNYC 291
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 300 THHKPCXNGATCTNTGQSYTCSCRPGYTSSCEIENECDANPCXNGGSGCTDLENSYC 359
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 THHKPCXNGATCTNTGQSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSC 351
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 360 TCPPGFYGNKCELSAMTCADGPCFNGGRCRTDNDPGGYSRCRPLGYSGFNCCKIDYCSSS 419
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 352 TCPPGFYGNKCELSAMTCADGPCFNGGRCSDNDGGYTCHCPLGFSGFNCCKMDLCSSS 411
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 420 PCANGAQCVDLGNYSYICQCQAGFTGRHCDNDVDDCASPPCVNGGTCQDGVNDYSCTCPGG 479
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 412 PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 480 YNGKNCSTPVSRCENHNPCHNGATCHERSNRYVCEARGYGGLNCQFLLPEPPQGPVIVDF 539
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 472 YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQYGGGPNQCQFLLPEPPPGMVVDL 531
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAVVVCVRLKVQRHHQPEACRSETETMN 599
: : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 532 SERHMESQGGPFPWAVAGVWLVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGSETETMN 591
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 600 NLANCOREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLVHELK-NE 657
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 592 NLANCOREKDVSVSIIGATQIKNTNKKADFHGHAKESSFKVRYPTVDYNLVRDLKGDE 651
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 658 DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDVYSTSKDTKYQSVYVISE 717
: : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 652 ATVRDTHSKRDTKCQSQSLQEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVYVLSA 711
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 718 EKDECIATEV 728
Db 712 EKDECVIATEV 722

RESULT 15
US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
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```
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-5

Query Match      80.6%; Score 3346.5; DB 3; Length 713;
Best Local Similarity 78.5%; Pred. No. 6.2e-244;
Matches 574; Conservative 67; Mismatches 69; Indels 21; Gaps 8;

QY 1 MGRFLTLTALLSALLCRQVDGSGVFELKQLQEFVNKKGLLSNRNCRRGG-GPGGAGQQQ 59
Db 1 MGRSALALAVSALL--CQWSSGVFELKQLQEFVNKKGLLSNRNCRRGGSP-----P 52

QY 60 CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSPVDGAGGADPAFNSPIRFPF 119
Db 53 CACRTFFRVCLKHYQASVSPEPPCTYGSAVTAVLGVDSPSLPDGA-GIDPAFNSPIRFPF 111

QY 120 GFTWPGTFSLLIEALHTDSPDLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLK 179
Db 112 GFTWPGTFSLLIEALHTDSPDLATENPERLISRLTTQRH-TVGEWSQDLHSSGRTDLR 170

QY 180 YSYRFVCEHHYEGGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCCDE 239
Db 171 YSYRFVCEHHYEGGCSVFCRPRDDAFHFTCGERGEKMCDPGWKQYCTDPICLPGCCDD 230

QY 240 QHGFCDKPGECKRVLGVQGRYDCECIRYPGLHGTCCQPWQCNCQEGWGLFCNQDLNYC 299
Db 231 QHGYCDKPGECKRVLGVQGRYDCECIRYPGLHGTCCQPWQCNCQEGWGLFCNQDLNYC 290

QY 300 THHKPCNKGATCTNTGQSYTCSCRPGYTGSCEIEINECDANPCKNGGSCDTLENSYSC 359
Db 291 THHKPCRNATCTNTGQSYTCSCRPGYTGANCELEVECAPSPCKNGGSCDTLEDSYSC 350

QY 360 TCPPGFYGNCELSAMTCADGPCFNGGRCTDNPDGYSRCRCLPYSGFNCCKIDYCSSS 419
Db 351 TCPPGFYGNCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPAGFSGFNCCKIDLCSSS 410

QY 420 PCANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPGG 479
Db 411 PCSNGAKCVDLGNSYLCRCQTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGG 470

QY 480 YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGGLNCQFLLPEPPQGPVIVDF 539
Db 471 YTGKNCAPVSRCEHNPCHNGATCHQGRQRYMCECAQYGGANCFLLPEPPDLIVA-- 528

QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIYVCVRLKVQKRHHQPEACRSETETMN 599
Db 529 -----AQGSFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPDPGGETETMN 582

QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLVHELK-NE 657
Db 583 NLANCQREKDVSVIIIGATQIKNTNKKADFHGDHGDADKSSFKARYPTVDYNLIRDLKGDE 642

QY 658 DSVKEEHGKCEAKCETVDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717
Db 643 ATVRDAHAKRDTKCQSQSAGEEKSTSTLRGGEVDRKRPESVYSTSKDTKYQSVYVLSA 702

QY 718 EKDECIIATEV 728
Db 703 EKDECVIATEV 713
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:11:34 ; Search time 76.5563 Seconds  
(without alignments)  
3411.281 Million cell updates/sec

Title: US-09-783-931-2  
Perfect score: 4153  
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIATEV 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					% Query		Description	
Result No.	Score	Match	Length	DB ID				
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2	4119.5	99.2	727	2	AAW11719		Aaw11719 C-Delta-1	
3	4108	98.9	728	3	AAY79029		Aay79029 Chick del	
4	3494.5	84.1	723	2	AAW18353		Aaw18353 Prolifera	
5	3494.5	84.1	723	2	AAW75492		Aaw75492 Human del	
6	3494.5	84.1	723	2	AAW94498		Aaw94498 Human del	
7	3494.5	84.1	723	3	AAY83227		Aay83227 PRO172 Po	
8	3494.5	84.1	723	3	AAB33422		Aab33422 Human PRO	
9	3494.5	84.1	723	3	AAB24388		Aab24388 Human PRO	
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13	3494.5	84.1	723	6	ABO17788		Abo17788 Novel hum	
14	3494.5	84.1	723	6	ABU81042		Abu81042 Human PRO	
15	3494.5	84.1	723	6	ABU66742		Abu66742 Human PRO	
16	3494.5	84.1	723	6	ABU59823		Abu59823 Novel sec	
17	3494.5	84.1	723	6	ABO25013		Abo25013 Human sec	
18	3494.5	84.1	723	6	ABU67018		Abu67018 Human sec	
19	3494.5	84.1	723	6	ADA45865		Ada45865 Novel hum	
20	3494.5	84.1	723	6	ADA76296		Ada76296 Human PRO	
21	3494.5	84.1	723	6	ADA18946		Ada18946 Human PRO	
22	3494.5	84.1	723	6	ADA61569		Ada61569 Homo sapi	
23	3494.5	84.1	723	6	ADB19354		Adb19354 Novel hum	
24	3494.5	84.1	723	6	ADB27895		Adb27895 Human PRO	
25	3494.5	84.1	723	6	ADA86374		Ada86374 Novel hum	

26	3494.5	84.1	723	6	ADB15938	Adb15938 Human PRO
27	3494.5	84.1	723	6	ADA47724	Ada47724 Human PRO
28	3494.5	84.1	723	6	ADA67519	Ada67519 Human PRO
29	3494.5	84.1	723	6	ADB30526	Adb30526 Human PRO
30	3494.5	84.1	723	6	ADA85822	Ada85822 Novel hum
31	3494.5	84.1	723	6	ADA97034	Ada97034 Human PRO
32	3494.5	84.1	723	6	ADA79338	Ada79338 Human PRO
33	3494.5	84.1	723	6	ADA87477	Ada87477 Novel hum
34	3494.5	84.1	723	6	ADB16679	Adb16679 Human PRO
35	3494.5	84.1	723	6	ADA91771	Ada91771 Novel hum
36	3494.5	84.1	723	6	ADB14834	Adb14834 Human PRO
37	3494.5	84.1	723	6	ADB18795	Adb18795 Novel hum
38	3494.5	84.1	723	6	ADA94010	Ada94010 Human PRO
39	3494.5	84.1	723	6	ADB19906	Adb19906 Novel hum
40	3494.5	84.1	723	6	ADB13218	Adb13218 Human PRO
41	3494.5	84.1	723	6	ABO43321	Abo43321 Novel hum
42	3494.5	84.1	723	6	ADA74472	Ada74472 Human PRO
43	3494.5	84.1	723	6	ADB24705	Adb24705 Human PRO
44	3494.5	84.1	723	6	ADA82229	Ada82229 Human PRO
45	3494.5	84.1	723	6	ADA75192	Ada75192 Human PRO

ALIGNMENTS

RESULT 1  
AAW00876  
ID AAW00876 standard; protein; 740 AA.  
XX  
AC AAW00876;  
XX  
DT 28-APR-1997 (first entry)  
XX  
DE C-Delta-1 polypeptide (alternatively spliced variant).  
XX  
KW C-Delta-1; cell proliferation; nervous system disorder;  
KW tissue regeneration; Notch; cervix cancer; breast cancer;  
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.  
XX  
OS Gallus sp.  
XX  
FH Key Location/Qualifiers  
FT Domain 184..228  
FT /label= DSL  
FT Domain 229..261  
FT /label= EGF1  
FT Domain 262..292  
FT /label= EGF2  
FT Domain 293..332  
FT /label= EGF3  
FT Domain 333..370  
FT /label= EGF4  
FT Domain 371..409  
FT /label= EGF5  
FT Domain 410..447  
FT /label= EGF6  
FT Domain 448..485  
FT /label= EGF7  
FT Domain 486..523  
FT /label= EGF8  
FT Domain 524..534  
FT /label= EGF9  
FT 555..579  
FT /label= TM  
FT /note= "transmembrane domain"

WO9701571-A1.  
16-JAN-1997.  
28-JUN-1996; 96WO-US011178.  
28-JUN-1995; 95US-0000589P.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PA (UYVA ) UNIV YALE.  
XX  
PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;  
PI Gray GE;  
XX WPI; 1997-100159/09.  
DR N-PSDB; AAT58898.  
XX  
PT New vertebrate Delta protein, DNA and antibodies - for treating and  
PT preventing cancer, nervous system disorders and for tissue regeneration.  
XX  
PS Disclosure; Fig 2; 135pp; English.  
XX  
CC C-delta-1 polypeptide (AAW00876) is the chick homologue of Drosophila  
CC Delta, a protein that binds to Notch protein. Expression of C-Delta-1  
CC correlates with onset of neurogenesis. The C-delta-1 amino acid sequence  
CC was deduced from a cDNA clone (AAT58898) obtd. from chick stage 4-6  
CC embryos. A shorter version (AAW58877) of C-Delta-1, lacking the 12 C-  
CC terminal amino acids of the longer version, was also isolated, and mouse  
CC (AAW11720) and human (AAW11721- 38) Delta-1 polypeptides have been  
CC identified. Delta-1 proteins can be used to treat or prevent disorders  
CC characterised by increased Notch activity, such as cervical, breast, lung  
CC or colon cancer, melanoma or seminoma, and nervous system disorders or to  
CC promote tissue regeneration and repair  
XX  
SQ Sequence 740 AA;  
  
Query Match 100.0%; Score 4153; DB 2; Length 740;  
Best Local Similarity 100.0%; Pred. No. 7.2e-228;  
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
Db |||||  
1 MGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
  
Qy 61 DCKTFRVCLKHQYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNPFPFG 120  
Db |||||  
61 DCKTFRVCLKHQYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNPFPFG 120  
  
Qy 121 FTWPGTFSLIIEALHTDSPDLLTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180  
Db |||||  
121 FTWPGTFSLIIEALHTDSPDLLTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180  
  
Qy 181 SYRFVCDHEYHGGCVFCRPRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240  
Db |||||  
181 SYRFVCDHEYHGGCVFCRPRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240  
  
Qy 241 HGFCDKPECKCRVWQGRYCDCEIRYPGCLHGTCQQPWCNQCQEGWGLFCNQDLNYCT 300  
Db |||||  
241 HGFCDKPECKCRVWQGRYCDCEIRYPGCLHGTCQQPWCNQCQEGWGLFCNQDLNYCT 300  
  
Qy 301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYCT 360  
Db |||||  
301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYCT 360  
  
Qy 361 CPPGFYGNKNCELSAMTCADGPCFNGGRCCTDNPDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
Db |||||  
361 CPPGFYGNKNCELSAMTCADGPCFNGGRCCTDNPDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
  
Qy 421 CANGAQCVDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Db |||||  
421 CANGAQCVDLGNYSYICQCOAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
  
Qy 481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPQGPVIVDFT 540  
Db |||||  
481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPQGPVIVDFT 540  
  
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLLGCAAIIVCVRLKVQRHHQPEACRSSETMNN 600  
Db |||||  
541 EKYTEGQNSQFPWIAVCAGIILVLLGCAAIIVCVRLKVQRHHQPEACRSSETMNN 600

Qy 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEEDSV 660  
Db |||||  
601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEEDSV 660  
  
Qy 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDVSYSTSKDTKYQSVYVISEEKD 720  
Db |||||  
661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDVSYSTSKDTKYQSVYVISEEKD 720  
  
Qy 721 ECIATEV 728  
Db |||||  
721 ECIATEV 728  
  
RESULT 2  
AAW11719  
ID AAW11719 standard; protein; 727 AA.  
XX  
AC AAW11719;  
XX  
DT 28-APR-1997 (first entry)  
XX  
DE C-Delta-1 polypeptide.  
XX  
KW C-Delta-1; cell proliferation; nervous system disorder;  
KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;  
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.  
XX  
OS Gallus sp.  
XX  
FH Key Location/Qualifiers  
FT Domain 184..228  
FT /label= DSL  
FT Domain 229..261  
FT /label= EGF1  
FT Domain 262..292  
FT /label= EGF2  
FT Domain 293..332  
FT /label= EGF3  
FT Domain 333..370  
FT /label= EGF4  
FT Domain 371..409  
FT /label= EGF5  
FT Domain 410..447  
FT /label= EGF6  
FT Domain 448..485  
FT /label= EGF7  
FT Domain 486..523  
FT /label= EGF8  
FT Domain 524..534  
FT /label= EGF9  
FT Domain 555..579  
FT /label= TM  
FT /note= "transmembrane domain"  
XX  
PN WO9701571-A1.  
XX  
PD 16-JAN-1997.  
XX  
PF 28-JUN-1996; 96WO-US011178.  
XX  
PR 28-JUN-1995; 95US-0000589P.  
XX  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PA (UYVA ) UNIV YALE.  
XX  
PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;  
PI Gray GE;  
XX  
DR WPI; 1997-100159/09.  
DR N-PSDB; AAT58897.  
XX  
PT New vertebrate Delta protein, DNA and antibodies - for treating and  
PT preventing cancer, nervous system disorders and for tissue regeneration.

XX Disclosure; Fig 2; 135pp; English.

XX C-delta-1 polypeptide (AAW11719) is the chick homologue of Drosophila

CC Delta, a protein that binds to Notch protein. Expression of C-Delta-1

CC correlates with onset of neurogenesis. The C-delta-1 amino acid sequence

CC was deduced from a cDNA clone (AAT58897) obtd. from chick stage 4-6

CC embryos. An alternatively spliced variant (AAW00876) was also isolated,

CC and mouse (AAW11720) and human (AAW11721- 38) Delta-1 polypeptides have

CC been identified. Delta-1 proteins can be used to treat or prevent

CC disorders characterised by increased Notch activity, such as cervical,

CC breast, lung or colon cancer, melanoma or seminoma, and nervous system

CC disorders or to promote tissue regeneration and repair

XX

SQ Sequence 727 AA;

Query Match 99.2%; Score 4119.5; DB 2; Length 727;

Best Local Similarity 99.6%; Pred. NO. 5.7e-226;

Matches 725; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQLQEFVFNKGLLSNRNCCRGGGPGGAGQQQC 60

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQLQEFVFNKGLLSNRNCCRGGGPGGAGQQQC 60

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 DCKTFFRVCLKHYQASVSEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNPFPFG 120

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 DCKTFFRVCLKHYQASVSEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNPFPFG 120

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 FTWPGTFLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 FTWPGTFLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 SYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 SYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 241 HGFCDKPGECKCRVGNQGRYCDCEIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 241 HGFCDKPGECKCRVGNQGRYCDCEIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 301 HHKPCKNGATCTNTGQSYTCSCRPGYTGSCEIINECDANPCKNGGSCDTLENSYSCT 360

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 301 HHKPCKNGATCTNTGQSYTCSCRPGYTGSCEIINECDANPCKNGGSCDTLENSYSCT 360

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 361 CPPGFYGNCELSAMTCADGPCFNGGRCCTNDPGYSRCRPLGYSGFNCCKIDYCSSSP 420

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 361 CPPGFYGNCELSAMTCADGPCFNGGRCCTNDPGYSRCRPLGYSGFNCCKIDYCSSSP 420

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 421 CANGAQCDLGNYSYCQAGFTGRHCDNDVDDCASFPVNGGTCCQDGVNDYSCTCPPGY 480

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 421 CANGAQCDLGNYSYCQAGFTGRHCDNDVDDCASFPVNGGTCCQDGVNDYSCTCPPGY 480

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 481 NGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 481 NGKNCSTPVSRCENHPCNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIYVCVRLKVQKRHHQPEACRSETETMNN 600

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIYVCVRLKVQKRHHQPEACRSETETMNN 599

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSV 660

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 600 LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSV 659

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTKDTKYQSVYVISEKD 720

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 660 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTKDTKYQSVYVISEKD 719

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 721 ECIIATEV 728

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 720 ECIIATEV 727

RESULT 3

AAAY79029

ID AAAY79029 standard; protein; 728 AA.

XX

AC AAAY79029;

XX

DT 06-JUN-2000 (first entry)

XX

DE Chick delta protein amino acid sequence.

XX

KW Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;

KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;

KW tissue regeneration; liver cirrhosis; keloid formation; baldness;

KW inner ear disorder; chick.

XX

OS Gallus sp.

XX

PN WO200002897-A2.

XX

PD 20-JAN-2000.

XX

PF 13-JUL-1999; 99WO-US015817.

XX

PR 13-JUL-1998; 98US-0092513P.

PR 19-OCT-1998; 98US-0104834P.

XX

PA (UYVA ) UNIV YALE.

XX

PI Artavanis-Tsakonas S, Rand MD, Qi H;

XX

DR WPI; 2000-282852/24.

XX

PT New cleavage peptide, nucleic acids and antibodies useful for diagnosis,

PT prevention and treatment of cancer, disorders of central nervous system,

PT cirrhosis and psoriasis.

XX

PS Claim 1; Fig 3; 177pp; English.

XX

CC This sequence represents the chick delta protein amino acid sequence.

CC Delta is a toporythmic protein that contains a sequence which is cleaved

CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz

CC results in two fragments, a soluble amino terminal fragment consisting

CC essentially of the extracellular domain, and a membrane bound fragment

CC consisting of the transmembrane domain and the intracellular domain. The

CC soluble fragment is able to bind to Notch. Delta plays a key role in

CC differentiation, and therefore detection and measurement of delta

CC activation is important in the study of differentiation. The invention

CC relates to the delta cleavage peptides (the active fragment), and to

CC methods for detecting and measuring delta activation. Delta cleavage

CC peptides, and chimeric proteins are useful for modulating the activity of

CC Notch, delta or kuz or at least one of the signalling pathways in a cell

CC or organism, expressing Notch. By contacting a cell with kuz protein or

CC nucleic acid or its antibody, the activity or levels of delta protein is

CC modulated and vice versa. A delta cleavage peptide or its derivative

CC capable of binding kuz protein is useful for treating or preventing a

CC disease or disorder associated with increased delta activity or

CC expression such as cervical, breast, colon or lung cancer, melanoma or

CC seminoma in humans. A recombinant cell comprising a delta peptide is

CC useful for treating or preventing central nervous system disorders. A

CC delta cleavage peptide is useful for the diagnosis of diseases or

CC disorders associated with increased levels of Notch-delta protein binding

CC activity comprising measuring the ability of delta cleavage peptides in a

CC sample to bind kuz protein. A complex of delta protein and kuz is useful

CC for diagnosing or screening for the presence of, or predisposition to

CC developing a disease or disorder associated with aberrant levels of the

CC complex, comprising measuring the level or functional activity of the

CC complex or RNA encoding delta or kuz in a sample. The delta cleavage

CC peptide is also useful for promoting tissue regeneration and repair, for

CC treating liver cirrhosis, keloid formation, psoriasis, baldness and

CC degenerative or traumatic disorders of the sensory epithelium of the

XX inner ear

SQ Sequence 728 AA;

Query Match	98.9%;	Score 4108;	DB 3;	Length 728;
Best Local Similarity	99.0%;	Pred. No. 2.6e-225;		
Matches	721;	Conservative 1;	Mismatches 6;	Indels 0; Gaps 0;
Qy	1	MGGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGGPGGAGQQQC	60	
Dd	1	MGGRFLLTLALLSALLCRCQVDCSGVFELKQEFVNKKGLLSNRNCCRGGGPGGAGQQQC	60	
Qy	61	DKTFFRVCLKHYYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSNPPIRFPFG	120	
Dd	61	DKTFFRVCLKHYYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSNPPIRFPFG	120	
Qy	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRDILKY	180	
Dd	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRDILKY	180	
Qy	181	SYRFVCDHEYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	240	
Dd	181	SYRFVCDHEYHYGEGCSVFCRPRDDHFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ	240	
Qy	241	HGFCDKPGECKCRVWQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCT	300	
Dd	241	HGYCDKPGECKCRVWQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCT	300	
Qy	301	HHKPCKNGATCTNTGQSYTCSCRPGYTGSSEIEINECDANPCKNGGSCDLENSYSCT	360	
Dd	301	HHKPCKNGATCTNTGQSYTCSCRPGYTGSSEIEINECDANPCKNGGSCDLENSYSCT	360	
Qy	361	CPPGFYGNCELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCEKKIDYCSSSP	420	
Dd	361	CPPGFYGNCELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCEKKIDYCSSSP	420	
Qy	421	CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY	480	
Dd	421	CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCDDGVNDYSCTCPPGY	480	
Qy	481	NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT	540	
Dd	481	NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT	540	
Qy	541	EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN	600	
Dd	541	EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN	600	
Qy	601	LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSV	660	
Dd	601	LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSV	660	
Qy	661	KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKD	720	
Dd	661	KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKD	720	
Qy	721	ECIIATEV 728		
Dd	721	ECIIATEV 728		
RESULT 4				
AAW18353				
ID	AAW18353	standard; protein; 723 AA.		
XX	XX			
AC	AAW18353;			
XX	XX			
DT	11-FEB-1998	(first entry)		
XX	XX			
DE	Proliferation and differentiation suppression polypeptide.			
XX	XX			
KW	Proliferation; differentiation; suppression; human; delta-1; serrate-1;			
KW	blood cell; neuron; leukaemia; malignant tumour; immunosuppression.			
XX	XX			
OS	Homo sapiens.			
XX	XX			

FH	Key	Location/Qualifiers
FT	Peptide	1..21
FT	Protein	/label= Signal
FT		22..723
FT		/label= Differentiation_suppression_protein
XX	WO9719172-A1.	
PN		
XX	XX	
PD	29-MAY-1997.	
XX	XX	
PF	15-NOV-1996;	96WO-JP003356.
XX	XX	
PR	17-NOV-1995;	95JP-00299611.
PR	30-NOV-1995;	95JP-00311811.
XX	XX	
PA	(ASAH ) ASahi KASEI KOGYO KK.	
XX	XX	
PI	Sakano S, Itoh A;	
XX	XX	
DR	WPI; 1997-298110/27.	
DR	N-PSDB; AAT70174.	
XX	XX	
PT	Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress	
PT	proliferation and differentiation of undifferentiated human blood cells.	
XX	XX	
PS	Claim 15; Page 77-82; 114pp; Japanese.	
XX	XX	
CC	The present sequence represents a polypeptide which suppresses	
CC	proliferation and differentiation of undifferentiated cells such as	
CC	neurons and blood cells. The polypeptide may be used for the prevention	
CC	and control of disorders involving undifferentiated cells, such as	
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	
CC	after immunosuppression	
XX	XX	
SQ	Sequence 723 AA;	
Query Match 84.1%; Score 3494.5; DB 2; Length 723;		
Best Local Similarity 83.3%; Pred. No. 1.8e-190;		
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;		
Qy	1	MGGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60
Dd	1	MGRSICALALAVLSALL--CQWSSGVSFELKQEFVNKKGLLSNRNCCR---GGAGPPPC 54
Qy	61	DKTFFRVCLKHYYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSNPPIRFPFG 120
Dd	55	ACRTFFRVCLKHYYQASVSPEPPCTYGSATPVLGVDSFSLPDG--GGADSAFSNPPIRFPFG 113
Qy	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRDILKY 180
Dd	114	FTWPGTFSLIIEALHTDSPDDLATENPERLISRATQRHLTVGEEWSQDLHSSGRDILKY 173
Qy	181	SYRFVCDHEYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Dd	174	SYRFVCDHEYHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233
Qy	241	HGFCDKPGECKCRVWQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCT 300
Dd	234	HGFCDKPGECKCRVWQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCT 293
Qy	301	HHKPCKNGATCTNTGQSYTCSCRPGYTGSSEIEINECDANPCKNGGSCDLENSYSCT 360
Dd	294	HHKPCKNGATCTNTGQSYTCSCRPGYTGTATCELGIDECDDPSCKNGGSCDLENSYSCT 353
Qy	361	CPPGFYGNCELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCEKKIDYCSSSP 420
Dd	354	CPPGFYGNCELSAMTCADGPCFNGGRCSDSPDGGYSCRCPCVGYSGFNCEKKIDYCSSSP 413
Qy	421	CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480
Dd	414	CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 473
Qy	481	NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540

















XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;

PI Yuan J;

XX WPI; 2000-638201/61.

DR N-PSDB; AAA54105.

XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for

PT treating tumors including cancers of the breast and lung, leukemia and

PT for identifying compounds capable of inhibiting growth of neoplastic

PT cells.

XX Claim 31; Fig 8; 133pp; English.

PS Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their

XX agonists (preferably anti-PRO agonist antibody or a small molecule

CC mimicking the biological activity of PRO polypeptide) are useful in vitro

CC or in vivo for inhibiting the growth of a tumour cell. Compositions

CC comprising the PRO polypeptides are useful for inhibiting neoplastic cell

CC growth and for treating cancer including breast, ovarian, renal,

CC colorectal, uterine, prostate, lung, bladder, central nervous system

CC cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also

CC useful for treating other disorders such as neuronal, glial, astrocytal,

CC hypothalamic and other glandular, macrophagal, epithelial, stromal,

CC blastocoelic disorders and inflammatory, angiogenic and immunologic

CC disorders as well as being useful for identifying agonists to PRO

CC polypeptides by contacting the polypeptide with a candidate molecule and

CC monitoring biological activity mediated by the polypeptide

XX

SQ Sequence 723 AA;

Query Match 84.1%; Score 3494.5; DB 3; Length 723;

Best Local Similarity 83.3%; Pred. No. 1.8e-190;

Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKGLLSNRNCCRGGPGGAGQQQC 60

DB 1 MGSRCALALAVLSALL--CQWSSGSGVFELKLOEFVNKGLLGNRCCR----GGAGPPPC 54

QY 61 DCKTFFRVCLKHQASVSPEPPCTYGSAITPVLGANSFSVPDGGAGGADPAFSPNIRFPFG 120

DB 55 ACRTFFRVCLKHQASVSPEPPCTYGSATPVLGVDSPFLPDG--GGADSAFSPNIRFPFG 113

QY 121 FTWPGTFSLLIEALHTDSPDDLTNTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180

DB 114 FTWPGTFSLLIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY 173

QY 181 SYRFVCDHYHYGEGSVFCRPRDRDFGHFTCGERGEKVCNPGWKQYCTTEPICLPGCDEQ 240

DB 174 SYRFVCDHYHYGEGSVFCRPRDDAFGHFTCGERGEKVCNPGWKPYCTTEPICLPGCDEQ 233

QY 241 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300

DB 234 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 293

QY 301 HHKPKNGATCTNTGGSYTCSCRPGYTGSSCETIEINECDANPCKNSSCTDLENSYSCT 360

DB 294 HHKPKNGATCTNTGGSYTCSCRPGYTGATCLGIDECDPSPCKNGSGSCTDLENSYSCT 353

QY 361 CPPGFYGNCELSAMTCADGPCFNGGRCCTNDPGGYSRCRPLGYSGFNCEKKIDYCSSSP 420

DB 354 CPPGFYGNCELSAMTCADGPCFNGGRCSDSPDGGYSRCRCPVGYSGFNCEKKIDYCSSSP 413

QY 421 CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCCQDGVNDYSCTCPPGY 480

DB 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPCANGGTCRDGVNDFSCTCPPGY 473

QY 481 NGKNVSTPVSRCENPCHNGATCHERSNRYVCEARGYGGNLNCQFLLPBPQGPVIVDFT 540

DB 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCEARGYGGNCPQFLLPBPQPAVVDLT 533

QY 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAALVVCVRLKVQKRHHQPEACRSRETETMNN 600

DB 534 EK-LEGQGGPPFWAVCAGVILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN 592

QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSPVDYNLVHELKKNED- 658

DB 593 LANCQREKDISVSIIGATQIKNTNKKADFGHDSADKNGFKARYPAVDYNLVQDLKGGDT 652

QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717

DB 653 AVRDAHSKRDTKQPPQSGSSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712

QY 718 EKDECIATEV 728

DB 713 EKDECVIATEV 723

RESULT 11

AAU12344

ID AAU12344 standard; protein; 723 AA.

XX AAU12344;

XX 24-OCT-2001 (first entry)

XX Human PRO172 polypeptide sequence.

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;

KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;

KW A-peptide; factor VIIA; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200140466-A2.

XX

PD 07-JUN-2001.

XX

PF

XX

XX 01-DEC-2000; 2000WO-US032678.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 09-DEC-1999; 99US-0170262P.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2001-408281/43.  
DR N-PSDB; AAS21416.  
XX  
PT Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.  
XX  
PS Claim 12; Fig 346; 813pp; English.  
XX  
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expressions in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMcs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy  
XX  
SQ Sequence 723 AA;

Query Match 84.1%; Score 3494.5; DB 4; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1.8e-190;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQWSSGSGVFELKLQEFVNKKGLLGNRNCCR----GGAGPPPC 54

Qy 61 DCKTFFRVCLKHYQASVSPEPCTYGSAITPVLGANSFSPDGGAGADPAFSNPIRPPFG 120  
Db 55 ACRTFFRVCLKHYQASVSPEPCTYGSATPVLGVDSFSLPDG-GGADSAFSNPIRPPFG 113

Qy 121 FTWPGTFSLIIEALHTDSPDLLTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKY 180  
Db 114 FTWPGTFSLIIEALHTDSPDLLATENPERLISRLATORHLTVGEEWSQDLHSSGRTDLKY 173

Qy 181 SYRFVCDHEYHGGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQ 240  
Db 174 SYRFVCDHEYHGGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233

Qy 241 HGFCDKPGECKCRVGWQGRYCDICIRYPGCLHGTCQQPWCNCQEGWGGLFCNQDLNYCT 300  
Db 234 HGFCDKPGECKCRVGWQGRYCDICIRYPGCLHGTCQQPWCNCQEGWGGLFCNQDLNYCT 293

Qy 301 HHKPCKNGATCTNTGQSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDTLENSYSCT 360  
Db 294 HHKPCKNGATCTNTGQSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCT 353

Qy 361 CPPGFYKNCELSAMTCADGPCFNGGRCCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420  
Db 354 CPPGFYKICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSP 413

Qy 421 CANGAACVDLGNYSYCQCQAGFTGRHCDNDVDDCASFPFCVNGGTCDQGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPPGY 473

Qy 481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLEPPPPQGPVIVDPT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLEPPPGPAVVDLT 533

Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGFPFWAVCAGVILVLMLLGCAAVVVVCVRLRLQKHRPPADPCRGETETMNN 592

Qy 601 LANCOREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED- 658  
Db 593 LANCOREKDISVSIIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDT 652

Qy 659 SVKEEHGKCEAKCETVDSEAEK-SAVQLKSSDTSERKRPPDSVYSTSKDTKYQSVYVISE 717  
Db 653 AVRNAHSKRDTKCPQGSSEGEKGTPTTLRGGEASERKRPPDSGCGSTSKOTKYQSVYVISE 712

Qy 718 EKDECIATEV 728  
Db 713 EKDECVIATEV 723

RESULT 12  
AAB53064  
ID AAB53064 standard; protein; 723 AA.  
XX  
AC AAB53064;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO172, SEQ ID NO:2.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US000219.  
XX  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 14-MAY-1999; 99US-0134287P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
XX



PA (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NP, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2001-090793/10.  
DR N-PSDB; AAC97368.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or angiogenic  
PT disorders, such as atherosclerosis, wounds or cancer.  
XX  
PS Claim 69; Fig 2; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof. PRO  
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to screen  
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map  
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene  
CC therapy. PRO nucleic acids can also be used to produce transgenic animals  
CC useful for the development and screening of potential therapeutic agents.  
XX The present sequence represents a PRO protein of the invention  
SQ Sequence 723 AA;

Query Match 84.1%; Score 3494.5; DB 4; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1.8e-190;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRQVDGSGVFELKQEFVNNKGLLSNRNCCRGGPGGAGQQQC 60  
DB 1 MGSRCALALAVLSALL--CQWSSGVFELKQEFVNNKGLLGNRNCCR-----GGAGPPPC 54

QY 61 DCKTFFRVCLKHYSQASVSEPPCTYGSAITPVLGANSFSVPDGGAGADPAFSPNIRFPFG 120  
DB 55 ACRTFFRVCLKHYSQASVSEPPCTYGSAVTPVLGVDSFSLPDG--GGADSAFSPNIRFPFG 113

QY 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRATQRHLAVGEWSQDLHSSGRTDLKY 180  
DB 114 FTWPGTFSLLIEALHTDSPDDLATENPERLISRATQRHLTVGEWSQDLHSSGRTDLKY 173

QY 181 SYRFVCDHYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKQGYCTEPTCLPGCDEQ 240  
DB 174 SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKPYCTEPTCLPGCDEQ 233

QY 241 HGFCDKPGECKCRVWGQGRYCDCEIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 300  
DB 234 HGFCDKPGECKCRVWGQGRYCDCEIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 293

QY 301 HHKPKNGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCKNGGSCDTLENSYSCT 360

Db 294 HHKPKNGATCTNTGQSYTCSRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCT 353  
QY 361 CPPGFYGNKNCELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCCKIDYCSSSP 420  
Db 354 CPPGFYGKICELSAMTCADGPCFNGGRCSDSPDGYSRCRCPGVYSGFNCCKIDYCSSSP 413  
QY 421 CANGAQCVDLGNYSYICQCAQFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRQDGVNDFSTCTPPGY 473  
QY 481 NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
QY 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGFPWVAVCAGVILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN 592  
QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658  
Db 593 LANCQREKDISISVIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGGDT 652  
QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Db 653 AVRDAHRSKRDTCQPPQSGSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISE 712  
QY 718 EKDECIIATEV 728  
Db 713 EKDECVIATEV 723

RESULT 13  
ABO17788  
ID ABO17788 standard; protein; 723 AA.  
XX ABO17788;  
AC ABO17788;  
XX  
DT 26-AUG-2003 (first entry)  
XX Novel human secreted and transmembrane protein PRO172.  
DE Human; secreted and transmembrane protein; PRO; antiinflammatory;  
XX antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
KW TNF-alpha release; cell proliferation; cell differentiation;  
KW gene expression modulator; proteoglycan release; cytokine release;  
KW tumour; inflammatory disease; organ failure; atherosclerosis;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
KW bioreactor; tissue typing.  
XX Homo sapiens.  
OS  
XX US2003032156-A1.  
XX 13-FEB-2003.  
XX  
PF 06-MAY-2002; 2002US-00140474.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-341980/32.  
DR N-PSDB; ACD24025.  
XX  
PT New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, axquired immunodeficiency  
PT syndrome (AIDS), or cancer.  
XX  
PS Claim 12; Fig 346; 660pp; English.  
XX  
CC The invention describes an isolated nucleic acid (I) comprising, or which  
CC has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences  
CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor viia, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This is the amino acid sequence of a novel human secreted and  
CC transmembrane PRO polypeptide  
XX  
SQ Sequence 723 AA;

Query Match 84.1%; Score 3494.5; DB 6; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1.8e-190;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7

Qy 1 MGGRFLTLALLSALLCRCQVDGSGVFELKIQEFVNKKLLSNRNCCRGGPGGAGQQC 60  
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Db 1 MGSRCALAVLSALL--CQWSSGVFELKIQEFVNKKGLLGNRNCCR---GGAGPPPC 54

Qy 61 DCKTFRVCLKHQASVSPEPCTYCSAITPVLGANSFSVPDGAAGADPAFSNPIRFPFG 120  
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Db 55 ACRTFRVCLKHQASVSPEPCTYCSAVTPVLGVDVSFSLPDG-GGADSAFSNPIRFPFG 113

Qy 121 FTWPGTFSLIIIEALTHDSDPDLTENPERLISRLATQRHLAVGEWSQDLHSSGRDTDLY 180  
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Qy 181 SYRFVCDEHYHGECSCVFCRPBRDRFGHTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240

Db 174 SYRFVDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPNWGKGPYCTEPICLPGCDEQ 233  
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Db 234 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 293  
Qy 301 HHKPCKNKGATCTNTGQSYTCSRPGYTGSSECEIEINECDANPCKNGGSCDTLSENSYCT 360  
Db 294 HHKPCKNKGATCTNTGQSYTCSRPGYTGATCELGIDECDFSPCKNGGSCDTLSENSYCT 353  
Qy 361 CPPGFYGNCELSAMTCADGCFNGGRCCTDNPDDGGYSCRPLGYSGFNCCEKKIDYCSSSP 420  
Db 354 CPPGFYKICELSAMTCADGCFNGGRCSDSPDDGGYSCRCPVGYSGFNCCEKKIDYCSSSP 413  
Qy 421 CANGAQCVDLGNSYICQCAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPGGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPPGY 473  
Qy 481 NGKNCSPTVSRCEHNPCHNGATCHERSNRYVCECARGYGGCLNCQFLLPEPPQGPIVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGPPFWAVACAGVILVLMLLLGCAAIVVCVRLQLQHRPPADPCRGETETMNN 592  
Qy 601 LANCQREKDISISVIGATQIKNTNKKVDFFHSDNS-DKNGYKVRYPSVDYNLVHELKVED- 658  
Db 593 LANCQREKDISVSIIGATQIKNTNKKADFHGDHSDAKNGFKARYPAVDYNLVQDLKGDDT 652  
Qy 659 SVKBEHGKCEAKCETYDSEABEK-SAVQLKSSDTSERKRPDSSVYSTSKOTKYQSVYVISE 717  
Db 653 AVRDAHAKRDTKCQPPQSSGEEKGTPTTLRGGEASERKRPDSGCSTSKOTKYQSVYVISE 712  
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Db 713 EKDECVIATEV 723  
RESULT 14  
ABU81042  
ID ABU81042 standard; protein; 723 AA.  
XX  
AC ABU81042;  
XX  
DT 23-JUN-2003 (first entry)  
XX  
DE Human PRO polypeptide #173.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;  
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
KW hearing loss; coagulation disorder; stroke; heart attack; cardiant;  
KW antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;  
KW antirheumatic; auditory; cerebroprotective; angiogenic.  
XX  
OS Homo sapiens.  
XX  
PN US2003004311-A1.  
XX  
PD 02-JAN-2003.  
XX  
PF 19-DEC-2001; 2001US-00028072.  
XX  
PR 18-JUN-1997; 97US-0049911P.  
PR 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059352P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 24-SEP-1997; 97US-0059836P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 17-OCT-1997; 97US-0062287P.  
PR 17-OCT-1997; 97US-0063755P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063082P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 27-OCT-1997; 97US-0063327P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 28-OCT-1997; 97US-0063550P.  
PR 28-OCT-1997; 97US-0063561P.  
PR 29-OCT-1997; 97US-0063704P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 29-OCT-1997; 97US-0063735P.  
PR 29-OCT-1997; 97US-0063738P.  
PR 03-NOV-1997; 97US-0064248P.  
PR 07-NOV-1997; 97US-0064809P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 17-NOV-1997; 97US-0065846P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 24-NOV-1997; 97US-0066453P.  
PR 24-NOV-1997; 97US-0066511P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 11-DEC-1997; 97US-0069212P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 23-JAN-1998; 98US-0072320P.  
PR 04-FEB-1998; 98US-0073612P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.



PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
XX  
PA (GETH ) GENENTECH INC.  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-352836/33.  
DR N-PSDB; ACA67166.  
XX  
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid  
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or  
PT heart attack.  
XX  
PS Claim 12; Fig 346; 643pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a medicament  
CC useful in the treatment of diabetes, bone and/or cartilage disorders  
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,  
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders  
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells, tissues or  
CC serum, and for affinity purification of PRO from recombinant cell culture  
CC or natural sources. ABU80870-ABU8144 represent the human PRO  
CC polypeptides of the invention. Note: The sequence data for this patent  
CC was obtained in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsDIDentry.html  
XX  
SQ Sequence 723 AA;

Query Match 84.1%; Score 3494.5; DB 6; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1.8e-190;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy 1 MGGRFLLTLLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCR---GGAGPPPC 54  
Qy 61 DCKTFFRVLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDAGGADPAFSNPIRFPFG 120  
Db 55 ACRTFFRVLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDG--GGADSAFSNPIRFPFG 113  
Qy 121 FTWPGETSLIIEALHTDSPDDLTNTENPERLISRLATQRLHVAVGEWSQDLHSSGRTDLKY 180  
Db 114 FTWPGETSLIIEALHTDSPDDLATENPERLISRLATQRLHTVGEWSQDLHSSGRTDLKY 173  
Qy 181 SYRFVCDHHYGECSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
Db 174 SYRFVCDHHYGECSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233

Qy 241 HGFCDKPGECKCRVWGQRYCDECIRYPGCLHGTCOOPWQCNCQEGWGGLFCNQDLNYCT 300  
Db 234 HGFCDKPGECKCRVWGQRYCDECIRYPGCLHGTCOOPWQCNCQEGWGGLFCNQDLNYCT 293  
Qy 301 HHKPCKNGATCTNTGGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCITDLENSYSCT 360  
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Qy 361 CPPGFYGNCELSAMTCADGPCFNGGRCCTDNPDDGYSRCRPLGYSGFNCCKKIDYCS SSP 420  
Db 354 CPPGFYGKI CELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCCKKIDYCS SSP 413  
Qy 421 CANGAQCVDLGSNYICQCOAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASPPCANGGTCRDGVNDFSCTCPPGY 473  
Qy 481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLPELPPGPAVV DLT 533  
Qy 541 EKYTEGONSQFPWIAVCAGIILVMLLLGCAAIVVCLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGFPFWAVCAGVILVMLLLGCAAVVVCLRLQKRRPPADPCRGETETMNN 592  
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Db 593 LANCOREKDISVSIIGATQIKNTNKKADFHGHDHADKNGFKARYPAVDYNLVQDLKGDDT 652  
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RESULT 15  
ABU66742  
ID ABU66742 standard; protein; 723 AA.  
AC ABU66742;  
XX 23-MAY-2003 (first entry)  
DE Human PRO polypeptide #173.  
XX Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.  
XX Homo sapiens.  
OS  
XX US2003036180-A1.  
PN 20-FEB-2003.  
PD 09-MAY-2002; 2002US-00143114.  
PF 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.





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Qy	361	CPPGFYG	KNCELSAMTCADG	PCFNGGRCTDNP	DGGYSCRCPLGY	SGFENCEKKIDYCS	SSP 420	
Db	354	CPPGFYG	KICELSAMTCADG	PCFNGGRCSDS	PDGGYSCRCPCV	GYSGFENCEKKIDYCS	SSP 413	
Qy	421	CANGAQCV	DLGNSYICQCQAG	FTGRHCDNVD	DCASFPVCVNGGT	CQDGVNDYSCTC	PPGY 480	
Db	414	CSNGAKCV	DLGDAYLCRCQAG	FSGRHCDNVD	DCASSPCANGGT	CRDGVNDFSC	TPPGY 473	
Qy	481	NGKNCST	TPVSRCEHNPCH	NGATCHERSNR	YVCECARGYG	GLNCQFLLPEPP	QGPVIVDFT 540	
Db	474	TGRNCSA	PVSRCEHAPCH	NGATCHERGH	RYVCECARGY	GGPNCQFLLPEL	PPGPAVVDLT 533	
Qy	541	EKYTEG	QNSQFPPIAVCA	GIILVLM	LLGCAAVV	CVRLKVQKRHHQ	PEACRSETETMNN 600	
Db	534	EK-LEG	QGGPFPWVAVCA	GVILVLM	LLGCAAVV	CVRLQLK	HRPPADPCRGETETMNN 592	
Qy	601	LANCQRE	KDISISVIGATQ	IKNTNKKVD	FHSDNS-DKNGY	KVRYPSVDYN	LVHELKNE	D- 658
Db	593	LANCQRE	KDISVSIIGATQ	IKNTNKKAD	FHGDHSADKNG	FKARYPAVDYN	LVQDLKGD	DT 652
Qy	659	SVKEH	GKCEAKCETYD	SEAEK-SAVQL	KSSDTSERKR	PD	SVYSTSKDTKYQSVY	VISE 717
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Qy	718	EKDECI	IATEV	728				
Db	713	EKDEC	VIATEV	723				

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 73.3366 Seconds  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4153	100.0	728	9 US-09-908-322-2	Sequence 2, Appli
2	4153	100.0	728	10 US-09-783-931-2	Sequence 2, Appli
3	4142.5	99.7	729	14 US-10-417-719-8	Sequence 8, Appli
4	3495.5	84.2	721	9 US-09-908-322-5	Sequence 5, Appli
5	3495.5	84.2	721	10 US-09-783-931-5	Sequence 5, Appli
6	3495.5	84.2	721	15 US-10-042-865-109	Sequence 109, App
7	3494.5	84.1	723	9 US-09-828-366-21	Sequence 21, Appli
8	3494.5	84.1	723	9 US-09-995-593A-9	Sequence 9, Appli
9	3494.5	84.1	723	14 US-10-028-072-346	Sequence 346, App
10	3494.5	84.1	723	14 US-10-140-808-346	Sequence 346, App
11	3494.5	84.1	723	14 US-10-121-049-346	Sequence 346, App
12	3494.5	84.1	723	14 US-10-123-904-346	Sequence 346, App
13	3494.5	84.1	723	14 US-10-140-470-346	Sequence 346, App

14	3494.5	84.1	723	14	US-10-175-746-346	Sequence 346, App
15	3494.5	84.1	723	14	US-10-176-918-346	Sequence 346, App
16	3494.5	84.1	723	14	US-10-176-921-346	Sequence 346, App
17	3494.5	84.1	723	14	US-10-137-865-346	Sequence 346, App
18	3494.5	84.1	723	14	US-10-140-474-346	Sequence 346, App
19	3494.5	84.1	723	14	US-10-142-431-346	Sequence 346, App
20	3494.5	84.1	723	14	US-10-143-114-346	Sequence 346, App
21	3494.5	84.1	723	14	US-10-140-002-346	Sequence 346, App
22	3494.5	84.1	723	14	US-10-142-419-346	Sequence 346, App
23	3494.5	84.1	723	14	US-10-241-476-27	Sequence 27, Appl
24	3494.5	84.1	723	14	US-10-123-262-346	Sequence 346, App
25	3494.5	84.1	723	14	US-10-142-423-346	Sequence 346, App
26	3494.5	84.1	723	14	US-10-121-050-346	Sequence 346, App
27	3494.5	84.1	723	14	US-10-141-755-346	Sequence 346, App
28	3494.5	84.1	723	14	US-10-143-032-346	Sequence 346, App
29	3494.5	84.1	723	14	US-10-123-108-346	Sequence 346, App
30	3494.5	84.1	723	14	US-10-123-236-346	Sequence 346, App
31	3494.5	84.1	723	14	US-10-123-261-346	Sequence 346, App
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33	3494.5	84.1	723	14	US-10-140-928-346	Sequence 346, App
34	3494.5	84.1	723	14	US-10-121-045-346	Sequence 346, App
35	3494.5	84.1	723	14	US-10-123-292-346	Sequence 346, App
36	3494.5	84.1	723	14	US-10-123-903-346	Sequence 346, App
37	3494.5	84.1	723	14	US-10-124-819-346	Sequence 346, App
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42	3494.5	84.1	723	14	US-10-127-825A-346	Sequence 346, App
43	3494.5	84.1	723	14	US-10-127-829A-346	Sequence 346, App
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45	3494.5	84.1	723	14	US-10-127-839A-346	Sequence 346, App

ALIGNMENTS

RESULT 1  
US-09-908-322-2  
; Sequence 2, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2

Query Match      100.0%; Score 4153; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQOQC 60
Db 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQOQC 60

QY 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNSPIRPFPG 120
Db 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNSPIRPFPG 120

QY 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATQRHLAGVEEWSQDLHSSGRTDLKY 180
Db 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATQRHLAGVEEWSQDLHSSGRTDLKY 180

QY 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240

QY 241 HGFCDKPGECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQLNLNYCT 300
Db 241 HGFCDKPGECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQLNLNYCT 300

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Db 301 HHKPCKNGATCTNTGQSYTCSRCRPGYTGSCEIEINECDANPCKNGGSCDTLENSYSCT 360

QY 361 CPPGFYKNCCELSAMTCADGPCFNGRCRTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSP 420
Db 361 CPPGFYKNCCELSAMTCADGPCFNGRCRTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSP 420

QY 421 CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480
Db 421 CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY 480

QY 481 NGKNCSTPVSRCENHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVDFT 540
Db 481 NGKNCSTPVSRCENHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVDFT 540

QY 541 EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600
Db 541 EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600

QY 601 LANCQREKDISISVIGATQIKNTNKKVDVPHSDNSDKNGYKVRYPVSDYNLVHELKNEDSV 660
Db 601 LANCQREKDISISVIGATQIKNTNKKVDVPHSDNSDKNGYKVRYPVSDYNLVHELKNEDSV 660

QY 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKD 720
Db 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKD 720

QY 721 ECIIATEV 728
Db 721 ECIIATEV 728
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RESULT 2

US-09-783-931-2

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; Sequence 2, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-931-2
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Query Match      100.0%; Score 4153; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQOQC 60
Db 1 MGRFLLTLALLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQOQC 60

QY 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNSPIRPFPG 120
Db 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFNSPIRPFPG 120

QY 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATQRHLAGVEEWSQDLHSSGRTDLKY 180
Db 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATQRHLAGVEEWSQDLHSSGRTDLKY 180

QY 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240

QY 241 HGFCDKPGECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQLNLNYCT 300
Db 241 HGFCDKPGECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQLNLNYCT 300

QY 301 HHKPCKNGATCTNTGQSYTCSRCRPGYTGSCEIEINECDANPCKNGGSCDTLENSYSCT 360
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Db 301 HHKPCXGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCXNGGSCDTLENSYSCT 360  
QY 361 CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
Db 361 CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
QY 421 CANGAQCVDLGNSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTC PPGY 480  
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Db 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600  
QY 601 LANQCREKDISISVIGATQIKNTNKKVDVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNE DSV 660  
Db 601 LANQCREKDISISVIGATQIKNTNKKVDVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNE DSV 660  
QY 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPRDSVYSTSKDTKYQSVYVISEEKD 720  
Db 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPRDSVYSTSKDTKYQSVYVISEEKD 720  
QY 721 ECIIATEV 728  
Db 721 ECIIATEV 728

RESULT 3

US-10-417-719-8  
; Sequence 8, Application US/10417719  
; Publication No. US20030180784A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF  
; FILE REFERENCE: MBIO1997-002CP2M  
; CURRENT APPLICATION NUMBER: US/10/417,719  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US/09/568,218  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 08/872,855  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 08/832,633  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 729  
; TYPE: PRT  
; ORGANISM: Gallus Gallus  
US-10-417-719-8

Query Match 99.7%; Score 4142.5; DB 14; Length 729;  
Best Local Similarity 99.9%; Pred. No. 1.5e-265;  
Matches 728; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNNKGLLSNRNCCRGSGGAGQQQC 60  
QY 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSPVDGAGGADPAFNPFRPFG 120  
Db 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSPVDGAGGADPAFNPFRPFG 120  
QY 121 FTWPGTFSLLIEALHTDSPDDLTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKY 180  
Db 121 FTWPGTFSLLIEALHTDSPDDLTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKY 180

QY 181 SYRFVCDEHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240  
Db 181 SYRFVCDEHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240  
QY 241 HGFCDKPGECKCRVGMQGRYCDDECIRYPGCLHGTCCQOPWQCNCQEGWGLFCNQDLNYCT 300  
Db 241 HGFCDKPGECKCRVGMQGRYCDDECIRYPGCLHGTCCQOPWQCNCQEGWGLFCNQDLNYCT 300  
QY 301 HHKPCXGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCXNGGSCDTLENSYSCT 360  
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QY 361 CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
Db 361 CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCEKKIDYCS SSP 420  
QY 421 CANGAQ-CVDLGNYSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTC PPG 479  
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QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539  
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QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMN 599  
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QY 600 NLANCOREKDISISVIGATQIKNTNKKVDVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNE DSV 659  
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Db 661 VKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPRDSVYSTSKDTKYQSVYVISEEK 720  
QY 720 DECIIATEV 728  
Db 721 DECIIATEV 729

RESULT 4

US-09-908-322-5  
; Sequence 5, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392



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Db 235 HHGYCDKPGCKCRVGMQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYC 294

QY 300 THHKPCNGATCTNTGQSYTCSRCRPGYTGSSCEIEINECDANPCKNGGSCDTLENSYSC 359
    |||||:|||||
Db 295 THHKPCNGATCTNTGQSYTCSRCRPGYTGSNCEIEVNECDANPCKNGGSCDLENSYTC 354

QY 360 TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSS 419
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Db 355 SCPPGFYGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCCKIDYCSSN 414

QY 420 PCANGAQCVDLGNSYICQCAQAGTGRHCDNVDNDCASFPCVNGGTCQDGVNDYSTCPCPG 479
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QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
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Db 475 YIGKNCSPITKCEHNPCHNGATCHERNRNVVCCQARGYGGNNCQFLLPE--EKPVVVDL 532

QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMN 599
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Db 533 TEKYTEGQSGQFPWIAVCAGIVLVLMLLGCAAVVVCVRVRVQKRRHQPEACRGETMTN 592

QY 600 NLANCQREKDISISVIGATQIKNTNKKVDPHSD-NSDKNGYKVRYPSPVDYNLVHELKNE 658
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Db 593 NLANCQREKDISISVIGTQIKNTNKKIDFLSESNNEKNKYKPRYPSPVDYNLVHELKNE 652

QY 659 SVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSPVYSTSKDTKYQSVYVISEE 718
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QY 719 KDECIATEV 728
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Db 712 KDECIATEV 721
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RESULT 6

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US-10-042-865-109
; Sequence 109, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
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; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 109
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-10-042-865-109

Query Match      84.2%; Score 3495.5; DB 15; Length 721;
Best Local Similarity 82.2%; Pred. No. 9e-223;
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVKKGLLSNRNCCRGGPGG-AGQQQ 59
    ||: ||| :|||: ||: ||: |||: ||||| ||||| ||||| |||||
Db 1 MGQRMLTLLVLSAVL--CQISCSGLFELRLQEFVKKGLLGNMNCR---PGSLASLQR 55

QY 60 CDCKTFFRVCLKHYQASVSPEPPCTYGSATPVLGANSFSVPDAGGADPAFSPNIRFPF 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 56 CECKTFFRICLKHYSQNSVSPEPPCTYGGAVTPVLGTNSFVVPE-SSNADPTFSNIRFPF 114

QY 120 GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRTDLK 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 GFTWPGTFSLIIEAIIHADSDADDLNTENPERLISRATQRHLTVGEWSQDLHSSDRTELK 174

QY 180 YSYRFVCDHEYVYGECSVFRCPRDRDFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDE 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 YSYRFVCDHEYVYGECSDYCRPRDDAFGHFSCGEKGLCNPGWKGLYCTEPICLPGCDE 234

QY 240 QHGFCDKPGCKCRVGMQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYC 299
    ||:|||||
Db 235 HHGYCDKPGCKCRVGMQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYC 294

QY 300 THHKPCNGATCTNTGQSYTCSRCRPGYTGSSCEIEINECDANPCKNGGSCDTLENSYSC 359
    |||||:|||||
Db 295 THHKPCNGATCTNTGQSYTCSRCRPGYTGSNCEIEVNECDANPCKNGGSCDLENSYTC 354

QY 360 TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSS 419
    :|||||
Db 355 SCPPGFYGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCCKIDYCSSN 414

QY 420 PCANGAQCVDLGNSYICQCAQAGTGRHCDNVDNDCASFPCVNGGTCQDGVNDYSTCPCPG 479
    |||||:|||||
Db 415 PCANGARCEDLGNSYICQCEGFGSRNCDNLDCTSFPCQNGGTCQDGINDYSTCPCPG 474

QY 480 YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
    ||||| :||:|||||
Db 475 YIGKNCSPITKCEHNPCHNGATCHERNRNVVCCQARGYGGNNCQFLLPE--EKPVVVDL 532

QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMN 599
    |||||:|||||
Db 533 TEKYTEGQSGQFPWIAVCAGIVLVLMLLGCAAVVVCVRVRVQKRRHQPEACRGETMTN 592

QY 600 NLANCQREKDISISVIGATQIKNTNKKVDPHSD-NSDKNGYKVRYPSPVDYNLVHELKNE 658
    |||||:|||||
Db 593 NLANCQREKDISISVIGTQIKNTNKKIDFLSESNNEKNKYKPRYPSPVDYNLVHELKNE 652

QY 659 SVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSPVYSTSKDTKYQSVYVISEE 718
    ||||| ||||| :||: |||||
Db 653 SPKEERSKCEAKCSSNDSDEVDNSVHSK-RDSSERRRPDSAYSTSKDTKYQSVYVISDE 711
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; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081695  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081818  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082999  
; PRIOR FILING DATE: 1998-04-24  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084637  
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; PRIOR APPLICATION NUMBER: 60/085338  
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; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085579  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/086414  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/086430  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088730  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088741  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088810  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088858  
; PRIOR FILING DATE: 19/98-06-11  
; PRIOR APPLICATION NUMBER: 60/089532  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089599  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089947  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/090349  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090429  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090445  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090538

; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
  
Query Match 84.1%; Score 3494.5; DB 14; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1e-222;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;  
  
Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQWSSGVFELKQLQEFVNKKGLLGNRNCCR----GGAGPPPC 54  
  
Qy 61 DKTFFRVCLKHVQASVSPPEPCTYGSAITPYLGANSFSVPDGGAGDPAFSPNIRFPFG 120  
Db 55 ACRTFFRVCLKHVQASVSPPEPCTYGSAVTPVLGVDSFSLPDG-GGADSAFSPNIRFPFG 113  
  
Qy 121 FTWPGTFSLIIEALHTDSPDDLTTHENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKY 180  
Db 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKY 173  
  
Qy 181 SYRFVCDEHYYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQ 240  
Db 174 SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKPYCTEPICLPGCDEQ 233  
  
Qy 241 HGFCDKPGECKRVGMQGRYCDCEIRYPGCLHGTCCQPWCNQCQEGWGLFCNQDLNYCT 300  
Db 234 HGFCDKPGECKRVGMQGRYCDCEIRYPGCLHGTCCQPWCNQCQEGWGLFCNQDLNYCT 293  
  
Qy 301 HHKPCKNGATCTNTQGSYTCSCRPGYTGSSCEIEINECDANPCXNGGSCDTLENSYSCT 360  
Db 294 HHKPCKNGATCTNTQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCT 353  
  
Qy 361 CPPGFYGNCELSAMTCADGPCFNGGRCTDNPBGYSRCRPLGYSGFENCEKKIDYCSSSP 420  
Db 354 CPPGFYKICELSAMTCADGPCFNGGRCSDSPDGYSCRCPVGYSGFENCEKKIDYCSSSP 413  
  
Qy 421 CANGAQCVDLGNYSICQCOAGFTGRHCDDNVDDCASFPVNGGTCCQDGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGY 473  
  
Qy 481 NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNQCQFLLPELPPGPAVVDLT 533  
  
Qy 541 EKYTEGONSQFPWIAVCAGIILVLMLLLGCAAIVCVRLKVKQRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGPFPWAVCAGVILVLMLLLGCAAVVVVCVRLRLQKHRPPADPCRGETETMNN 592  
  
Qy 601 LANQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNEED- 658  
Db 593 LANQREKDISISVIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGGDT 652  
  
Qy 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVVYVISE 717  
Db 653 AVRDAHSKRDTKCQPGSSGEEKGTPTTLRGSEASERKRPDSGCSSTSKDTKYQSVVYVISE 712  
  
Qy 718 EKDECIIATEV 728  
Db 713 EKDECVIATEV 723

RESULT 10  
US-10-140-808-346  
; Sequence 346, Application US/10140808  
; Publication No. US20030017563A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-346

Query Match 84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60
Db 1 MGSRCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLNRRNCCR----GGAGPPPC 54

QY 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSVPDGGAGGADPAFSPNPIRFPFG 120
Db 55 ACRTFFRVCLKHQYQASVSPPEPCTYGSATPVLGVDSFSLPDG-GGADSAFSPNPIRFPFG 113

QY 121 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 173

QY 181 SYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQ 240
Db 174 SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300
Db 234 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 293

QY 301 HHKPCXNGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCXNGGSCDTLENSYSCT 360
Db 294 HHKPCXNGATCTNTGQSYTCSRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCT 353

QY 361 CPPGFYGNCELSAMTCADGPCFNGGRCTDNDGGYSCRCPLGYSGFNCCKIDYCSSSP 420
Db 354 CPPGFYGNCELSAMTCADGPCFNGGRCSDSPGGYSCRCPLGYSGFNCCKIDYCSSSP 413

QY 421 CANGAQCVDLGNSYICQCAQFTGRHCDNDVDDCASFPVCVNGGTCCQGVNDYSCTCPPGY 480
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASFPVCANGGTCTRDGVNDFSCTCPPGY 473

QY 481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPBPQGPVIVDFT 540
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLPBPQGPVAVVDLT 533

QY 541 EKYTEGONSQFPMIYAVCAGIILVLMLLGCAIVVYVRLKVKQRHHQBPACRSETETMNN 600
Db 534 EK-LEGQGGPPFVAVCAGVILVLMLLGCAIVVYVRLQLKRPAPPCRGETETMNN 592

QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPVSDYNLVHELKNEED- 658
Db 593 LANCQREKDISISVIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDT 652

QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSDTSEKRRPDSVYSTSKDTKYQSVYVISE 717
Db 653 AVRDAHSKRDTXCPQGGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISE 712

QY 718 EKDECIATEV 728
Db 713 EKDECVIATEV 723

RESULT 11
US-10-121-049-346
; Sequence 346, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-346

Query Match 84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60
Db 1 MGSRCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLNRRNCCR---GGAGPPPC 54

QY 61 DCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSVPDGGAGGADPAFSPNPIRFPFG 120
Db 55 ACRTFFRVCLKHQYQASVSPPEPCTYGSATPVLGVDSFSLPDG-GGADSAFSPNPIRFPFG 113

QY 121 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 180
Db 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRATQRLHVLAVGEWSQDLHSSGRTDLKY 173

QY 181 SYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQ 240
Db 174 SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

QY 241 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300
Db 234 HGFCDKPGECKCRVGMQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 293

QY 301 HHKPCXNGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCXNGGSCDTLENSYSCT 360

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Db      294 HHKPCKNGATCTNTGQSYTCSRPGYTGATCELGDDECDPSPCKNGGSCDTLENSYSCT 353
QY      361 CPPGFYGNCELSAMTCADGPCFNGGRCTDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420
Db      354 CPPGFYGIKCELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSP 413
QY      421 CANGAQCVDLGNSYICQCAAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480
Db      414 CSNGAKCVDLGDAYLCRCQAQGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGY 473
QY      481 NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540
Db      474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533
QY      541 EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600
Db      534 EK-LEGQGGPPFWAVCAGVILVLMLLGCAAVVVCVRLQLQKRPADPCRGSETETMNN 592
QY      601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658
Db      593 LANCQREKDISVSIIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGGDDT 652
QY      659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSEKRPDSVYSTSKDTKYQSVYVISE 717
Db      653 AVRDAHSKRDTKCQPOGSSGEEKGPTTTLRGGEASERKRPSDSCSTSKDTKYQSVYVISE 712
QY      718 EKDECIIATEV 728
Db      713 EKDECVIATEV 723
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RESULT 12

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US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346
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Query Match      84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-22;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

QY      1 MGRFLLTLALLCRQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC 60
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Db      1 MGRSCALALAVLSALL--CQWSSGVFELKLQEFVNKKGLLSNRNCCR---GGAGPPPC 54
QY      61 DCKTFFRVCLKHYQASVSPPEPPCTYGSAITPVLGANSFSVPDAGGADPAFSNPIRPFPG 120
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      55 ACRTFFRVCLKHYQASVSPPEPPCTYGSAVTPVLGVDSFSLPDG-GGADSAFSNPIRPFPG 113
QY      121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      114 FTWPGTFSLLIEALHTDSPDDLATENPERLISRLATORHLTVGEWSQDLHSSGRTDLKY 173
QY      181 SYRFVCDEHYYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      174 SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233
QY      241 HGFCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 300
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      234 HGFCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 293
QY      301 HHKPCKNGATCTNTGQSYTCSRPGYTGSSCEIINECDANPCKNGGSCDTLENSYSCT 360
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      294 HHKPCKNGATCTNTGQSYTCSRPGYTGATCELGDDECDPSPCKNGGSCDTLENSYSCT 353
QY      361 CPPGFYGNCELSAMTCADGPCFNGGRCTDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      354 CPPGFYGIKCELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSP 413
QY      421 CANGAQCVDLGNSYICQCAAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      414 CSNGAKCVDLGDAYLCRCQAQGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGY 473
QY      481 NGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533
QY      541 EKYTEGONSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600
      ||| ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      534 EK-LEGQGGPPFWAVCAGVILVLMLLGCAAVVVCVRLQLQKRPADPCRGSETETMNN 592
QY      601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658
Db      593 LANCQREKDISVSIIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGGDDT 652
QY      659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSEKRPDSVYSTSKDTKYQSVYVISE 717
      |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db      653 AVRDAHSKRDTKCQPOGSSGEEKGPTTTLRGGEASERKRPSDSCSTSKDTKYQSVYVISE 712
QY      718 EKDECIIATEV 728
      |||||:|||||
Db      713 EKDECVIATEV 723
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RESULT 13

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US-10-140-470-346
; Sequence 346, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
```



```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-346

Query Match      84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy      1  MGRFLLTLALLSALLCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60
Db      1  MGSRCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLGNRNCCR----GGAGPPPC 54

Qy      61  DCKTFFRVCLKHYSVSEPPCTYGSAITPVLGANSFSVPDAGGADPAFNSPIRFPFG 120
Db      55  ACRTFFRVCLKHYSVSEPPCTYGSVAVTPVLGVSFSLPDG--GGADSAFNSPIRFPFG 113

Qy      121  FTWPGTFSLLIEALHTDSPDDLTATENPERLISRLATQRLHLAGVEWSQDLHSSGRTDLKY 180
Db      114  FTWPGTFSLLIEALHTDSPDDLTATENPERLISRLATQRLHLAGVEWSQDLHSSGRTDLKY 173

Qy      181  SYRFVCDHYHYGEGCSVFCRPRDDRFHFTTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db      174  SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

Qy      241  HGFCDKPGECKRCRVGWQGRYCDICIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 300
Db      234  HGFCDKPGECKRCRVGWQGRYCDICIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 293

Qy      301  HHKPCKNKGATCTNTGQSYTCSRPGYTGSSECEIENECDANPCKNKGGSCDTLENSYSCT 360
Db      294  HHKPCKNKGATCTNTGQSYTCSRPGYTGSSECEIENECDANPCKNKGGSCDTLENSYSCT 353

Qy      361  CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCCKIDYCSSSP 420
Db      354  CPPGFYGNKCELSAMTCADGPCFNGGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP 413

Qy      421  CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480
Db      474  TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGPNQCQFLLPPEPPAVVDLT 533

Qy      541  EKYTEGQNSQFPWIAVCAGIILVLLGLCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600
Db      534  EK-LEGQGGFPFWAVACAGVILVLLGLCAAIVVCVRLQLQKRPAPADPCRGETETMNN 592

Qy      601  LANQOREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNE- 658
Db      593  LANQOREKDISISVIGATQIKNTNKKADFHGSHADKNGFKARYPAVDYNLVQDLKGGDT 652

Qy      659  SVKEEHGKCEAKCETYDSEAEK-SAVQLKSDTSERKRPDSVYSTSKTKYQSVYVISE 717
Db      653  AVRDAHSKRDTKCQPGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKTKYQSVYVISE 712

Qy      718  EKDECIIATEV 728
Db      713  EKDECVIATEV 723
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RESULT 14  
US-10-175-746-346  
; Sequence 346, Application US/10175746

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; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-346

Query Match      84.1%; Score 3494.5; DB 14; Length 723;
Best Local Similarity 83.3%; Pred. No. 1e-222;
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;

Qy      1  MGRFLLTLALLSALLCQVDGSGVFELKQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60
Db      1  MGSRCALALAVLSALL--CQWSSGVFELKQEFVNKKGLLGNRNCCR----GGAGPPPC 54

Qy      61  DCKTFFRVCLKHYSVSEPPCTYGSAITPVLGANSFSVPDAGGADPAFNSPIRFPFG 120
Db      55  ACRTFFRVCLKHYSVSEPPCTYGSVAVTPVLGVSFSLPDG--GGADSAFNSPIRFPFG 113

Qy      121  FTWPGTFSLLIEALHTDSPDDLTATENPERLISRLATQRLHLAGVEWSQDLHSSGRTDLKY 180
Db      114  FTWPGTFSLLIEALHTDSPDDLTATENPERLISRLATQRLHLAGVEWSQDLHSSGRTDLKY 173

Qy      181  SYRFVCDHYHYGEGCSVFCRPRDDRFHFTTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240
Db      174  SYRFVCDHYHYGEGCSVFCRPRDDAFGHFTTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 233

Qy      241  HGFCDKPGECKRCRVGWQGRYCDICIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 300
Db      234  HGFCDKPGECKRCRVGWQGRYCDICIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCT 293

Qy      301  HHKPCKNKGATCTNTGQSYTCSRPGYTGSSECEIENECDANPCKNKGGSCDTLENSYSCT 360
Db      294  HHKPCKNKGATCTNTGQSYTCSRPGYTGSSECEIENECDANPCKNKGGSCDTLENSYSCT 353

Qy      361  CPPGFYGNKCELSAMTCADGPCFNGGRCCTDNDGGYSCRCPLGYSGFNCCKIDYCSSSP 420
Db      354  CPPGFYGNKCELSAMTCADGPCFNGGRCSDSPDGGYSCRCPLGYSGFNCCKIDYCSSSP 413

Qy      421  CANGAQCVDLGNSYICQCAQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480
Db      414  CSNGAKCVDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGGY 473

Qy      481  NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPPEPPQGPVVDFT 540
Db      474  TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGPNQCQFLLPPEPPAVVDLT 533

Qy      541  EKYTEGQNSQFPWIAVCAGIILVLLGLCAAIVVCVRLKVQKRHHQPEACRSETETMNN 600
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Db 534 EK-LEGQGGPFPWAVACAGVILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN 592  
QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNEID- 658  
Db 593 LANCQREKDISVSIIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDT 652  
QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Db 653 AVRDAHSKRDTKCQPQSGSGEEKGTPTTLRGGEASERKRPDSCSTSKDTKYQSVYVISE 712  
QY 718 EKDECIIATEV 728  
Db 713 EKDECVIATEV 723

RESULT 15  
US-10-176-918-346  
; Sequence 346, Application US/10176918  
; Publication No. US20030027275A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C382  
; CURRENT APPLICATION NUMBER: US/10/176,918  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-918-346

Query Match 84.1%; Score 3494.5; DB 14; Length 723;  
Best Local Similarity 83.3%; Pred. No. 1e-222;  
Matches 609; Conservative 47; Mismatches 64; Indels 11; Gaps 7;  
QY 1 MGRFLLTLALLSALLRCQVDGSGVFELKLQEFVNNKGLLSNRNCCRGGGPGGAGQQQC 60  
Db 1 MGSRCALALAVLSALL--CQWSSGVFELKLQEFVNNKGLLGNRNCCR----GGAGPPPC 54  
QY 61 DCKTFFRVCLKHYQASVSPPEPCTYGSAITPVLGANSFSPVDPGAGGADPAFSPNIRFPFG 120  
Db 55 ACRTFFRVCLKHYQASVSPPEPCTYGSAVTPVLGVDSPSLPDG-GGADSAFSPNIRFPFG 113  
QY 121 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEWSQDLHSSGRTDLKY 180  
Db 114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATORHLTVGEWSQDLHSSGRTDLKY 173  
QY 181 SYRFVCDHEYHGGCSVFCRPRDRDFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
Db 174 SYRFVCDHEYHGGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233  
QY 241 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 300

Db 234 HGFCDKPGECKCRVWGQGRYCDDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCT 293  
QY 301 HHKPCKNGATCTNTGGSYTCSCRPGYTGSSCEIBEINECDANPCKNKGSGSCTDLENSYCT 360  
Db 294 HHKPCKNGATCTNTGGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSGCTDLENSYCT 353  
QY 361 CPPGFYGNCELSAMTCADGPFCFNGGRCCTDNDPGGYSRCRPLGYSGFNCCEKKIDYCSSSP 420  
Db 354 CPPGFYGKI CELSAMTCADGPFCFNGGRCSDSPDGGYSRCRCPVGYSGFNCCEKKIDYCSSSP 413  
QY 421 CANGAQCVDLGNYSYCQCQAGFTGRHCDDNVDDCASFPVCVNGGTCDQGVNDYSCTCPPGY 480  
Db 414 CSNGAKCVDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCTRDGVNDFSCTCPPGY 473  
QY 481 NGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVDFT 540  
Db 474 TGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLT 533  
QY 541 EKYTEGONSQFPWIAVCAGIILVLMLLLGCAAVVVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 534 EK-LEGQGGPFPWAVACAGVILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN 592  
QY 601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNEID- 658  
Db 593 LANCQREKDISVSIIGATQIKNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDT 652  
QY 659 SVKEEHGKCEAKCETYDSEAEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Db 653 AVRDAHSKRDTKCQPQSGSGEEKGTPTTLRGGEASERKRPDSCSTSKDTKYQSVYVISE 712  
QY 718 EKDECIIATEV 728  
Db 713 EKDECVIATEV 723

Search completed: November 29, 2004, 13:41:58  
Job time : 77.3366 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 18.2447 Seconds  
(without alignments)  
3839.238 Million cell updates/sec

Title: US-09-783-931-2  
Perfect score: 4153  
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVVYVISEEKDECIATEV 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4153	100.0	728	2 I50719	C-Delta-1 - chicke
2	3407	82.0	722	2 I48324	DELTA-like 1 - mou
3	1897	45.7	685	2 JC7570	Delta-4 protein -
4	1863	44.9	686	2 JC7569	Delta-4 protein -
5	1559.5	37.6	833	2 S19087	gene Delta protein
6	1555.5	37.5	832	2 A31246	neurogenic protein
7	1555.5	37.5	880	2 S00670	neurogenic repetit
8	1332.5	32.1	1220	2 A56136	jagged protein pre
9	1126.5	27.1	1408	2 S16148	gene serrate prote
10	815	19.6	2524	2 A35844	Xotch protein - Af
11	806.5	19.4	2437	2 S42612	transmembrane prot
12	793	19.1	2531	2 T31070	notch homolog - se
13	787.5	19.0	1064	2 A40136	fibropellin Ia - s
14	784.5	18.9	2703	1 A24420	notch protein - fr
15	781	18.8	1203	2 A49175	Notch B protein -
16	781	18.8	2531	2 A46019	notch-1 protein -
17	776.5	18.7	2471	2 A49128	cell-fate determin
18	776	18.7	2352	2 T30201	Notch homolog prot
19	775.5	18.7	2531	2 S18188	notch protein homo
20	754	18.2	2139	2 A35672	crumbs protein - f
21	754	18.2	2555	2 A40043	notch protein homo
22	749	18.0	2321	2 S78549	notch3 protein - h
23	732	17.6	2318	2 S45306	notch 3 protein -
24	709.5	17.1	1964	2 T09059	notch4 - mouse
25	694.5	16.7	570	2 A48836	fibropellin C prec
26	694.5	16.7	861	2 A48825	Notch homolog Motc
27	660	15.9	473	2 A56175	adhesive plaque pr
28	627	15.1	1372	2 T25933	hypothetical prote
29	626	15.1	385	2 S53718	homeotic protein d

30	625	15.0	1722	2 E89753	protein F11C7.4 [i
31	618	14.9	385	2 A54785	preadipocyte facto
32	601	14.5	383	2 S53716	delta-like homeoti
33	591.5	14.2	1295	2 A32901	glp1 protein precu
34	589.5	14.2	1429	2 S06434	homeotic protein 1
35	583	14.0	1531	2 T42218	slit-1 protein hom
36	577.5	13.9	1025	2 T42626	secreted leucine-r
37	573.5	13.8	1469	2 B36665	slit protein 2 pre
38	573.5	13.8	1480	2 A36665	slit protein 1 pre
39	561	13.5	308	2 JC7125	epidermal growth f
40	551	13.3	1687	2 T30176	EGF repeat transme
41	538.5	13.0	601	2 T22025	hypothetical prote
42	538.5	13.0	601	2 D89711	protein F40E10.4 [
43	520	12.5	1523	2 T13953	MEGF5 protein - ra
44	506	12.2	387	2 B49175	Motch A protein -
45	487.5	11.7	3623	2 T08618	intrinsic factor-B

ALIGNMENTS

RESULT 1  
I50719  
C-Delta-1 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50719  
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.  
Nature 375, 787-790, 1995  
A;Title: Expression of a Delta homologue in prospective neurons in the chick.  
A;Reference number: I50719; MUID:95319507; PMID:7596411  
A;Accession: I50719  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-728 <HEN>  
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g8824  
C;Superfamily: delta-4 protein; EGF homology  
F;299-332/Domain: EGF homology <EGX1>  
F;339-370/Domain: EGF homology <EGF1>  
F;416-447/Domain: EGF homology <EGX2>  
F;454-485/Domain: EGF homology <EGF>  
F;492-523/Domain: EGF homology <EGF3>

Query Match	100.0%;	Score	4153;	DB	2;	Length	728;
Best Local Similarity	100.0%;	Pred.	No. 3.3e-242;				
Matches	728;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC	60				
Db	1	MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC	60				
QY	61	DKTFFRVCLKHQASVSPPEPCTYGSATPVLGANSFVSPDGAGGADPAFNPFRPFPG	120				
Db	61	DKTFFRVCLKHQASVSPPEPCTYGSATPVLGANSFVSPDGAGGADPAFNPFRPFPG	120				
QY	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHVLAVGEWSQDLHSSGRTDLKY	180				
Db	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHVLAVGEWSQDLHSSGRTDLKY	180				
QY	181	SYRFVCDHEYHGGCSVFCRPRDDRFHFTGGERGEKVCNPGWKQYCTEPICLPGCDEQ	240				
Db	181	SYRFVCDHEYHGGCSVFCRPRDDRFHFTGGERGEKVCNPGWKQYCTEPICLPGCDEQ	240				
QY	241	HGFCDKPGECKCRVWGQGRYCDICIRYPGLHGTCCQPPWCNCQEGWGLFCNQDLNYCT	300				
Db	241	HGFCDKPGECKCRVWGQGRYCDICIRYPGLHGTCCQPPWCNCQEGWGLFCNQDLNYCT	300				
QY	301	HHKPCXNGATCTNTGQGSYTCSCRPGYTSSCBIEINECDANPCXNGGSCDTLENSYSCT	360				
Db	301	HHKPCXNGATCTNTGQGSYTCSCRPGYTSSCBIEINECDANPCXNGGSCDTLENSYSCT	360				
QY	361	CPPGFYGNCELSAMTCADGPGCFNGGRCCTDNPDGGYSCRCPLGYSGFNCKKIDYCSSSP	420				

Db 361 CPFGYGNCELSAMTCADGPCFNGGRCRDTNPDGGYSCRCPLGYSGFNCEKKIDYCSSP 420

Qy 421 CANGAQCVDLGNYSYICQCQAGFTGRHCDDNVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480

Db 421 CANGAQCVDLGNYSYICQCQAGFTGRHCDDNVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480

Qy 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVDFT 540

Db 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVDFT 540

Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQRHHQPEACRSETETMNN 600

Db 541 EKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQRHHQPEACRSETETMNN 600

Qy 601 LANQREKDISISVIGATQIKNTNKKVDFFHSDNSDKNGYKVRYPSPVDYNLVHELKNEHSV 660

Db 601 LANQREKDISISVIGATQIKNTNKKVDFFHSDNSDKNGYKVRYPSPVDYNLVHELKNEHSV 660

Qy 661 KEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKD 720

Db 661 KEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKD 720

Qy 721 ECIATEV 728

Db 721 ECIATEV 728

RESULT 2

I48324

DELTA-like 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48324

R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.

Development 121, 2407-2418, 1995

A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin

A;Reference number: I48324; MUID:95401858; PMID:7671806

A;Accession: I48324

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-722 <RES>

A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065

C;Genetics:

A;Gene: Dll1

C;Superfamily: delta-4 protein; EGF homology

F;331-362/Domain: EGF homology <EGF2>

F;446-477/Domain: EGF homology <EGF>

F;484-515/Domain: EGF homology <EGF1>

Query Match 82.0%; Score 3407; DB 2; Length 722;

Best Local Similarity 79.5%; Pred. No. 2.2e-197;

Matches 581; Conservative 71; Mismatches 67; Indels 12; Gaps 6;

Qy 1 MGRFLTLTALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGQQQ 59

Db 1 MGRSALALAVVSALL--CQWSSGVFELKLQEFVNKKGLLSNRNCCRGSGP-----P 52

Qy 60 CDKTFFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSVPDGAGGADPAFSPNPIRFPF 119

Db 53 CACRTFFRVCLKHQASVSPPEPCTYGSAVTPVLGVDSPSLPDGA-GIDPAFSPNPIRFPF 111

Qy 120 GFTWPGTFSLIIIEALHTDSPDILTENPERLISRATORHLAVGEWSQDLHSSGRTDLK 179

Db 112 GFTWPGTFSLIIIEALHTDSPDLATENPERLISRLTTQRLHTVGEWSQDLHSSGRTDLR 171

Qy 180 YSRFVCDHEYHGGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDE 239

Db 172 YSRFVCDHEYHGGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDD 231

Qy 240 QHGFCDKPGECKCRVGMQGRYDDECIRYPGCLHGTCCQPWCNQCQEGWGLFCNQDLNYC 299

Db 232 QHG YCDKPGECKCRVGMQGRYDDECIRYPGCLHGTCCQPWCNQCQEGWGLFCNQDLNYC 291

Qy 300 THHKPCKNGATCTNTGQGSYTCSCRPGYTSSCEIINECDANPCKNGGSGCTDLENSYSC 359

Db 292 THHKPCRNATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSC 351

Qy 360 TCPPGFYGNCELSAMTCADGPCFNGGRCRDTNPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419

Db 352 TCPPGFYGNCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCSGS 411

Qy 420 PCANGAQCVDLGNYSYICQCQAGFTGRHCDDNVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479

Db 412 PCSNGAKCVDLGNYSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471

Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVVD 539

Db 472 YTGKNCAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL 531

Qy 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQRHHQPEACRSETETMN 599

Db 532 SERHMESQGGPFPWAVCAGVVLVLLLLLGCAAVVVCVRLKIQKHQPPPEPCGGETETMN 591

Qy 600 NLANCQREKDISISVIGATQIKNTNKKVDFFHSDN-SDKNGYKVRYPSPVDYNLVHELK-NE 657

Db 592 NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAKKSSFVKRYPTVDYNLVRLDLKDE 651

Qy 658 DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717

Db 652 ATVRDTHSKRDTKCSQSSSAGEEKIAPTLRGGEIPDRKRPSVYSTSKDTKYQSVYVLSA 711

Qy 718 EKDECIATEV 728

Db 712 EKDECVIATEV 722

RESULT 3

JC7570

Delta-4 protein - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C;Accession: JC7570

R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J

J. Biochem. 129, 27-34, 2001

A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A;Reference number: JC7569; MUID: 21064937; PMID:11134954

A;Accession: JC7570

A;Molecule type: mRNA

A;Residues: 1-685 <YON>

A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894

C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re

ates the Notch signaling, the growth or differentiation of vascular endothelial cells.

C;Genetics:

A;Gene: delta-4

C;Superfamily: delta-4 protein; EGF homology

C;Keywords: transmembrane protein

Query Match 45.7%; Score 1897; DB 2; Length 685;

Best Local Similarity 48.2%; Pred. No. 1.1e-106;

Matches 352; Conservative 112; Mismatches 195; Indels 72; Gaps 18;

Qy 11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQCDCKTFFRVCL 70

Db 14 LLLVALWQORAAGSGVFQLQEFINERGVLASGPRCEPG-----CRTFFRVCL 62

Qy 71 KHYQASVSPPEPCTYGSAITPVLGANSFSVPDGAGGADPAFSPNPIRFPFGFTWPGTFSLI 130

Db 63 KHFAQVAVSP-GPCTFGTVSTPVLGTNSFAVRDSSGGG---RNPLQLPFNFTWPGTFSLI 118

Qy 131 IEALHTDSPDILTTE--NPERLISRATORHLAVGEWSQDLHSSGRTDLKYSYRFPVDE 188

Db 119 IEAWHAPG-DDLRPEALPPDALISKIAIQGSLAVQNWLLDEQSTLTTLRLRYSYRVCISD 177

Qy 189 HYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQHGFCDKPG 248

Db 178 NYGDNCSRLCKKRNDHFGHYVCQPDGNLSCLPGWTGEYCCQPICLSGCHEQNGYCSKPA 237



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QY 249 ECKCRVWGQGRYCDICIRYPGLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPKNG 308
Db 238 ECLCRPGWQGRLCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHSPCKNG 297
QY 309 ATCTNTGQSYTCSCRPGYTGSSCEIEINECDANPCKNNGSCTDLENSYSCTCPPGYGK 368
Db 298 ATCSNSGQRSYTCRCRPGYTGVDCELESECDNSPCRNNGSCKDQEDGYHCLCPGYGL 357
QY 369 NCELSAMTCADGPCFNGGRCRTD-NPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQC 427
Db 358 HCEHSTLSCADSPCFNGGSCRERNQANYACECPNFTGSNCEKKVDRCTSNPCANGGQC 417
QY 428 VDLGNSYICQCAQAGTGRHCDNDVDDCASFPVCVNGGTQDQGVNDYSCTCPPGYNGKNCS- 486
Db 418 LNRGSPRMCRCRPGFTGTTCYELHVSDCARNPCAHGGTCHDLENGLMCTCPAGFSGRCEV 477
QY 487 -TPVSRCEHNPCHNGATCHE--RSNRYVCECARGYGGLNCGQLLPEPPQGPVIVDFTEKY 543
Db 478 RTSIDACASSPCFNRCATCYTDLSTDTFVCNCPYGFVGSRCFPPVGLPP----- 525
QY 544 TEGQNSQFPWIAVCAGI-ILVLMLLGCAIIVCVRLKVKQRHHQPEACRSETETMNNLA 602
Db 526 -----SFPWVAVSLGVGLAVLLVLLGMVAV-----RQLRLRRPD--DGSREAMNLS 572
QY 603 NCQREKDISISVIGATQIKNTNKKVDFHSD-NSDK-NGYKVRYPSVDYNLVHELKNEDSV 660
Db 573 DFQKD-----NLIPAAQLKNTNQKKELEVDGCLDKSNCCKQONHTLDYNLAPGLG---- 623
QY 661 KEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPD---SVYSTSKDTKYQSVYVISE 717
Db 624 ---RGTMPGKFPKSHDSKSLGEKAPLRLHS-----EKPECRISAICSPRDSMYQSVCLISE 674
QY 718 EKDECIATEV 728
Db 675 ERNECVIATEV 685

RESULT 4
JC7569
Delta-4 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7569
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7569
A;Molecule type: mRNA
A;Residues: 1-686 <YON>
A;Cross-references: UNIPROT:Q9DBU9; DDBJ:AB043893
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology

Query Match 44.9%; Score 1863; DB 2; Length 686;
Best Local Similarity 47.7%; Pred. No. 1.2e-104;
Matches 349; Conservative 107; Mismatches 206; Indels 70; Gaps 18;

QY 9 LALLSALLCRCQVDGSGVFELKQEFVNNKGLLSNRNCCRGGGPGGAGQQQCDCKTFFRV 68
Db 13 LLLAVLWPQQRAAGSGIFQLRLQEFVNQRGMLANGQSCFPG-----CRTFFRI 61

QY 69 CLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGTWPGTFS 128
Db 62 CLKHFQATFS-EGPCTFGNVSTPVLGTNSFVVRDKNSGSG---RNPLQLPFNFTWPGTFS 117

QY 129 LIIEALHTDSPDDLTTENP--ERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVC 186
Db 118 LNIQAWHTPG-DDLRPETSPGNSLISQIIIQGSLAVGKIWRTDEQNDTLRLSYSYRVIC 176
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QY 187 DEHYYGEGCSVFCRPRDRFRGHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQHGFCDK 246
Db 177 SDNYYGESCSRLCKKRDHDFGHYECQPDGSLSLCLPGWTGKYCDQPICLSGCHEQNGYCSK 236
QY 247 PGECKCRVWGQGRYCDICIRYPGLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPK 306
Db 237 PDECICRPGWQGRLCNECIPHNGCRHGTCIIPWQACADEGWGGLFCDQDLNYCTHSPCK 296
QY 307 NGATCTNTGQSYTCSCRPGYTGSSCEIEINECDANPCKNNGSCTDLENSYSCTCPPGY 366
Db 297 NGSTCSNSGPKGYTCTCLPGYTGEHCELGLSKCASNPGRNGGSKDQENSYHCLCPPGY 356
QY 367 GKNCELSAMTCADGPCFNGGRCRTD-NPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGA 425
Db 357 GQHCEHSTLTCADSPCFNGGSCRERNQNGSSYACECPNFTGSNCEKKVDRCTSNPCANGG 416
QY 426 QCVDLGNYSYICQCAQAGTGRHCDNDVDDCASFPVCVNGGTQDQGVNDYSCTCPPGYNGKN 485
Db 417 QCQNRGPSRTCRCRPGFTGTTCYELHISDCARSPCAHGGTCHDLENGVPVCTCPAGFSGRRC 476
QY 486 STPVSR--CEHNPCHNGATCHE--RSNRYVCECARGYGGLNCGQLLPEPPQGPVIVDFTE 541
Db 477 EVRITHDACASGPCFNGATCYTGLSPNPFVNCNCPYGFVGSRCFPPVGLPP----- 526
QY 542 KYTEGQNSQFPWIAVCAGIILVLMLLGCAIIVCVRLKVKQRHHQPEACRSETETMNNL 601
Db 527 -----SFPWVAVSLGVGLVLLVL-LVMVVVAVR---QLRLRRPD--DESREAMNNL 572
QY 602 ANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDK-NGYKVRYPSVDYNLVHELKNEDS 659
Db 573 SDFQXD-----NLIPAAQLKNTNQKKELEVDGCLDKSNCCKLQNHHTLDYNLAPGLLG--- 624
QY 660 VKEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRPD---SVYSTSKDTKYQSVYVVIS 716
Db 625 ----RGMPGKYPHSDKSLGEKVPRLHS-----EKPECRISAICSPRDSMYQSVCLIS 674
QY 717 EEKDECIATEV 728
Db 675 ERNECVIATEV 686
```

```
RESULT 5
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S19087
R;Muskhavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Reference number: S19087
A;Accession: S19087
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-833 <MUS>
A;Cross-references: UNIPROT:P10041; EMBL:Y00222
C;Genetics:
A;Gene: FlyBase:D1
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology <EGF1>
F;378-415/Domain: EGF homology <EGX1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
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Query Match 37.6%; Score 1559.5; DB 2; Length 833;
Best Local Similarity 42.4%; Pred. No. 2.4e-86;
Matches 292; Conservative 83; Mismatches 241; Indels 73; Gaps 14;

QY 11 LLSALLC---RCQVDGSGVFELKQEFVNNKGLLSNRNCCRGGGPGGAGQQQCDCKTFFR 67
Db 7 LLTAFICFTVIVQVHSSGSFELRLKYFSNDHRDNEGRCCSGESDGGATGKCLGSKCTRFR 66
```







R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2188-2201, 1990  
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential for  
A;Reference number: A36666; MUID:91099666; PMID:2125287  
A;Accession: A36666  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15,20-26,'A',28-1408 <FLE>  
A;Cross-references: GB:M35759; NID:G158605; PID:G158606  
C;Genetics:  
A;Gene: FlyBase:Ser  
A;Cross-references: FlyBase:FBgn0004197  
C;Keywords: glycoprotein; transmembrane protein  
F;1-84/Domain: signal sequence #status predicted <SIG>  
F;85-1408/Product: gene serrate protein #status predicted <MAT>  
F;85-1221/Domain: extracellular #status predicted <EXT>  
F;283-316/Domain: EGF homology <EG01>  
F;319-348/Domain: EGF homology <EG02>  
F;355-388/Domain: EGF homology <EG03>  
F;395-488/Domain: EGF homology #status atypical <EG04>  
F;495-526/Domain: EGF homology <EG05>  
F;533-608/Domain: EGF homology #status atypical <EG06>  
F;615-645/Domain: EGF homology <EG07>  
F;652-683/Domain: EGF homology <EG08>  
F;690-720/Domain: EGF homology <EG09>  
F;727-796/Domain: EGF homology #status atypical <EG10>  
F;803-834/Domain: EGF homology <EG11>  
F;841-876/Domain: EGF homology <EG12>  
F;883-914/Domain: EGF homology <EG13>  
F;921-952/Domain: EGF homology <EG14>  
F;997-1060/Region: cysteine-rich  
F;1222-1246/Domain: transmembrane #status predicted <TM1>  
F;1247-1408/Domain: intracellular #status predicted <INT>  
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn  
Query Match 27.1%; Score 1126.5; DB 2; Length 1408;  
Best Local Similarity 33.1%; Pred. No. 4e-60;  
Matches 226; Conservative 73; Mismatches 203; Indels 181; Gaps 16;  
Qy 9 LALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGSGPGGAGQQQ---CD-CKT 64  
Db 70 IALILILLVH-KISAAGNFELLEISNTNSHLNGYCC--GMPAELRATKTIIGCSPTT 126  
Qy 65 FFRVCLKHYQ-----ASVSPEPPCTYGSAITPVLGANSFSPVDGAGGADPAFNSPIRFPF 119  
Db 127 AFRULCKEYQTTEQGASIS--TGCSFGNATTKILGSSFVLSDPGVGA-----IVLPF 177  
Qy 120 GFTWPCTFSLIEAL---HTDSPDDLTTENPERLISRLATORHLAVGEESQDLHSSGRT 176  
Db 178 TFRWTKSFTLILQALDMYNTSPD-----AERLIBETSYSGVILPSPWKTLDHGRNA 231  
Qy 177 DLKYSYRFVCDHYHGECSVFCRPRDRDRFGHFTCGERGEKVCNPNWKQYCTEPICLPG 236  
Db 232 RITYRVRVQCAVYYNTTCTTCRPRDDQFGHYACGSEQKLCNLNGWQGVNCEEAIKAG 291  
Qy 237 CDEQHGFCDKPGECKCRVGNQGRYCDDECIRYPGCLHGTQO-QPWQCNCQEGWGGLFCNQD 295  
Db 292 CDPVHGKCDRPGECECRPGWRGPLCNECMVYPGCKHSGCSAWKCVCDTNWGGILCDQD 351  
Qy 296 LNYCTHHKPKNGATCTNTQGSY-----  
Db 352 LNFQGTHEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVEHPCATRPCRNGGTCTLKTS 411  
Qy 320 -----  
Db 412 NRTQAQVYRTSHGRSNMGRPVRSSSMRSLDHLRPEGQALNGSSSSGLVSLGLQIQQL 471  
Qy 320 ----TCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYCTCPPGFYGNKNCELSAM 375  
Db 472 APDFTCDCAAGWTGPTCEINIDECAGGPCEHGGTCIDLIGGPRCECPPPEWHGVDVCQVDVN 531  
Qy 376 TC-----ADGPCFNGGRCTDN 391

Db 532 ECEAPHSAGIAANALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECRNQ 591  
Qy 392 PDGGYSCRCPLGYSGFNCCEKKIDYCSSSPCANGAQCVDLGNYSYICQCQAGFTGRHCDNV 451  
Db 592 P-GSFACICKEGGWGVTCALNLDCCVGQ-CRNGATCIDLVNDYRCACASGFTGRDCETDI 649  
Qy 452 DDCAFSPCVNGGTCDQGVNDYSCTCPPGYNGKNCSTPVSRCHEHNPCHNGATCHERSNRYV 511  
Db 650 DECATSPCRNGGECVDMVGKFNCCICPLGYSGSLCEEAKENCTPSPCLEG-HCLNTPEGYY 708  
Qy 512 CECARGYGGNLNCQFLLP---EPP 531  
Db 709 CHCPPDRAGKHCEQLRPLCSQPP 731  
RESULT 10  
A35844  
Xotch protein - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 16-Aug-2004  
C;Accession: A35844  
R;Coffman, C.; Harris, W.; Kintner, C.  
Science 249, 1438-1441, 1990  
A;Title: Xotch, the Xenopus homolog of Drosophila notch.  
A;Reference number: A35844; MUID:90385285; PMID:2402639  
A;Accession: A35844  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: mRNA  
A;Residues: 1-2524 <COF>  
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: transmembrane protein  
F;146-177/Domain: EGF homology <EGX1>  
F;184-215/Domain: EGF homology <EGF1>  
F;222-254/Domain: EGF homology <EGF>  
F;456-487/Domain: EGF homology <EGX2>  
F;757-788/Domain: EGF homology <EGF3>  
F;1025-1056/Domain: EGF homology <EGX3>  
F;1924-1956/Domain: ankyrin repeat homology <AN1>  
F;1957-1989/Domain: ankyrin repeat homology <AN2>  
F;1991-2023/Domain: ankyrin repeat homology <AN3>  
F;2024-2056/Domain: ankyrin repeat homology <AN4>  
F;2057-2089/Domain: ankyrin repeat homology <AN5>  
Query Match 19.6%; Score 815; DB 2; Length 2524;  
Best Local Similarity 29.3%; Pred. No. 3.5e-41;  
Matches 190; Conservative 68; Mismatches 220; Indels 170; Gaps 22;  
Qy 17 CRCQVDGSGVF-ELKLQEFVNKKGLLSNRNCCRGSGPGGAGQQQCDCKTFFRVCLKHYQA 75  
Db 476 CICMPGYEGLYCETNIDECASNP-CLHNGKCI-----DKINEFRCDCTPFGSGLCQHDF 529  
Qy 76 SVSPEPPCTYGSAITPVLGANSFS--VPDGAGG-----ADPAFSNPIRFPFGFTWPCTF 127  
Db 530 DECTSTPCKNAGAKCLD--GPNSYTCQCTEGFTGRHCEQDINECIPDPCHYGTCKDGIATF 587  
Qy 128 SLIIEALHT-----  
Db 588 TCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYICTCPKGTGVCETKI----- 642  
Qy 157 QRHLAVGEESQDLHSSGR-TDLKYSYRFVCDHYHGECSVFCRPRD-----D 204  
Db 643 -----DDCASNLCDNGKCIDKIDGYECTCEPGYTGKLCNININECDSPCRNPGGTCKD 695  
Qy 205 RFGHFTC-----GERGEKV-CNPGWKQYC----- 228  
Db 696 QINGFTCVCPDGYHDMCLSEVNECNSNPCIHGACHDGVNGYKDCCEAGWSGNSCDINNN 755  
Qy 229 ---TEPICLPGDEQHGFC-DKPGE--CKRVWQGRYC----DECIRYPGCLHGTC--- 275  
Db 756 ECESNP-CMNG-----GTCKDMTGAYICTCKAGSGPNCQTNINECSSNPCLNHGTCIDD 809  
Qy 276 -----QQPWQCNCQEGWGGLFCNQD 295



Db 810 VAGYKNCMLPYTGAICEAVLAPCAGSPCKNGGRCKESEDFETFSCECPPGWQQTCEID 869

Qy 296 LNYCTHHKPKNGATCTNTGQSYTCSRPGYTGSCEIBEINECDANPCKNGGSCDTLEN 355

Db 870 MNECV-NRPCRNGATCQNT-NGSYKCNCKPGYTGRNCEMDIDDCQPNPCHNGGSCSDGIN 927

Qy 356 SYSCTCPPGFYGNKCELSAMTCADGPCFNGGRCTDNDGGYSRCRPLGYSGFNCEKKIDY 415

Db 928 MFFCNCAPFRGPKCEEDINECASNPCKNGANCTDCVN-SYTCTCQPGFSGIHCESNTPD 986

Qy 416 CSSSPCANGAQCVDLGNSYTCQCAQFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCT 475

Db 987 CTSSCFNGGTCIDGINTFTCQPPGFTGSYCOHDINECDSKPCLNGGTCQDSYGYKCT 1046

Qy 476 CPPGYNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNC 523

Db 1047 CPQGYTGLNCQLVRWCDSSPCKNGGKCWQTNNFYRCCKSGWTGVYC 1094

RESULT 11

S42612

transmembrane protein precursor - zebra fish

C;Species: Brachydanio rerio (zebra fish)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S42612

R;Bierkamp, C.; Campos-Ortega, J.A.

Mech. Dev. 43, 87-100, 1993

A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern

A;Reference number: S42612; MUID:94128602; PMID:8297791

A;Accession: S42612

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2437 <BIE>

A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g4338

C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

F;755-786/Domain: EGF homology <EGF1>

F;1023-1054/Domain: EGF homology <EGF>

F;1185-1216/Domain: EGF homology <EGF2>

F;1915-1947/Domain: ankyrin repeat homology <AN1>

F;1948-1980/Domain: ankyrin repeat homology <AN2>

F;1982-2014/Domain: ankyrin repeat homology <AN3>

F;2015-2047/Domain: ankyrin repeat homology <AN4>

F;2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 19.4%; Score 806.5; DB 2; Length 2437;

Best Local Similarity 27.3%; Pred. No. 1.1e-40;

Matches 190; Conservative 69; Mismatches 195; Indels 241; Gaps 26;

Qy 12 LSALLCRCQVDGSG-VPELKLQEFVNKKGLLSNRNCRGGG-----PGGAGQ 57

Db 582 VASFTCDCRPGYTGRLCETNINECLSQP-----CRNGGTCQDRENAYICTPKGTTG 633

Qy 58 QQC-----DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAG-----GA 107

Db 634 VNCEINIDCK-----RKPCDYGKCIDKINGYECVCEPGYSGSMCNINI 677

Qy 108 DPAFSNPIRFPFGFTWPCTFSLIIEALHTDSPDILTENPERLISRATQRHLAVGEWS 167

Db 678 DDCALNPCHN-----GGTC-----IDGVNSFTCLCPDGRDATCLSQH-----NECS 719

Qy 168 QD--LHSSGRDCLKYSYRFVFCDEHYHGECSV-----FCRPRDRFGHFTC 211

Db 720 SNPCIHSGCLDQIN-SYRCVCEAGWMGRNCIDINIECLSNPCVNGGTCK---DMTSGYLC 775

Qy 212 GERGEKVCNPGWKQYCTEPI-----CL--PGC-DEQHGFCDKPGECKCRVGMQGRYC 261

Db 776 -----TCRAGFSGPNQCMNINECASNPCLNQGSCIDDDVAGF-----KCNCLMPLYTGEVC 824

Qy 262 DE----CIRYPGCLHGTQ-----QPWQCNCQEGWGLFCNQDLNYCTHHKPKNGATCT 312

Db 825 ENVLAPCSRPCKNGGVCRESEDFQSFSCNCPAGWQGTCEVDINECVRN-PCTNGGVCE 883

Qy 313 NTQGSYTCSCRPGYTGSSCEIEINECDAN----- 342

Db 884 NL-RGGFQCRCPNGFTGALCENDIDDCENPNCSNGGVCQDRVNGFVCVCLAGFRGERCAE 942

Qy 343 -----PCKNGGSCDTLENSYSTCPCPPGFYGNKCELSAMTCADGPCFNGGRCTDN--- 391

Db 943 DIDECVSAPCRNGGNTDCVNSYTCSCPAGFSGNGEINTPDCTESSCFNGGTCVDGISS 1002

Qy 392 -----PDGG-----YSCRCPLGYSGFNCEKKIDYCS 417

Db 1003 FSCVCLPGFTGNYCQHDVNECDSRPCQNGGSCQDGYGTYKCTCPHGYTGLNCQSLVRWCD 1062

Qy 418 SSPCANG-----AQCV 429

Db 1063 SSPCKNGGSCWQOGASFTCCASGWTGIYCDVPSVSCEVAARQQGVSAVLCRHAGQCVD 1122

Qy 430 LGNSYICQCAQFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGYNGKNCSTPV 489

Db 1123 AGNTHLCRCQAGYTGSYCQEVDCEQPNPCQNGATCTDYLGGYSCECVPGYHGMNCSKEI 1182

Qy 490 SRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQ 524

Db 1183 NECLSQPCQNGGTCIDLVTYKCS CPRGTQGVHCE 1217

RESULT 12

T31070

notch homolog - sea urchin (Lytechinus variegatus)

C;Species: Lytechinus variegatus (variegated urchin)

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000

C;Accession: T31070

R;Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997

A;Title: Identification and localization of a sea urchin Notch homologue: insights into

A;Reference number: Z20966; MUID:97454256; PMID:9310331

A;Accession: T31070

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2531 <SHE>

A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1

C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 19.1%; Score 793; DB 2; Length 2531;

Best Local Similarity 30.6%; Pred. No. 7.3e-40;

Matches 184; Conservative 80; Mismatches 231; Indels 106; Gaps 23;

Qy 2 GGRFLLTLALLSALLCRCQV-----DGSGVFELK-----LQEFVNKKGLLSNRN 45

Db 495 GGYACICLTGTGTCLCETDINECSSNPCLNGASCDFITGRFECACLAGYTGTTCCQVNIDD 554

Qy 46 C----CRGGP--GGAGQQQCDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFS 99

Db 555 CQSSPCENGTCIDGVNQFTCLCETGYEGHRCEMDSDECASRPCMNGGVCEDLIGFYQCN 614

Qy 100 VPDGAGGADPAF-----SNPIRFPFGFTWPCTFSLIIEALHTDSPDILTENPERLISR 153

Db 615 CPVGTSGDNCEYNHYDCSSNP-----CVNDGTCVDGINEYTCMCHE----- 655

Qy 154 LATQRHLAVGEE---WSQDLHSSGR-TDLKYSYRFVFCDEHYHGECSVFCRPR----- 202

Db 656 --GYRGLNCEEDIDDCESRPCNNGGTCVDEVNGYHCLCPIGYH----DPPCMSNINECSS 709

Qy 203 -----DDRFHFTCGERGEKVCNPGWKQYCTEPI-----CLPG--CDEQHGFC 244

Db 710 NPCVNGGSGCHGVNEYSC-----ECMAGYTGTRCTDDDFDECSSNPCHGTCNDRHAFY 763

Qy 245 DKPGECKRVGMQGRYC---DECIRYPGLH-GTC---QQPWQCNCQEGWGLFCNQDL 296

Db 764 N-----CTCAQYTGTLNCEVNIDDCVDEP-CLNGGICIDEVNSFOCVCPQTfVGLLCETER 818

Qy 297 NYCTHHKPKNGATCT-NTQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCDTLEN 355

Db 819 SPCEDNQ-CQNGATCVSEDYAGYSCRCTSGFQGNFCDDDRNECLFSPCRNGGSCTNLEG 877



notch protein - fruit fly (Drosophila melanogaster)  
N;Alternate names: neurogenic repetitive locus protein  
C;Species: Drosophila melanogaster  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: A24420; A24768; S09358; A05267  
R;Kidd, S.; Kelley, M.R.; Young, M.W.  
Mol. Cell. Biol. 6, 3094-3108, 1986  
A;Reference number: A24420; MUID:87064624; PMID:3097517  
A;Accession: A24420  
A;Molecule type: DNA  
A;Residues: 1-2703 <KID>  
A;Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993  
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.  
Cell 43, 567-581, 1985  
A;Reference number: A24768; MUID:86079539; PMID:3935325  
A;Accession: A24768  
A;Molecule type: mRNA  
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,  
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044  
R;Tautz, D.  
Nucleic Acids Res. 17, 6463-6471, 1989  
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma  
A;Reference number: S09358; MUID:89385974; PMID:2780284  
A;Accession: S09358  
A;Molecule type: DNA  
A;Residues: 2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>  
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.  
Cell 40, 55-62, 1985  
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other  
A;Reference number: A05267; MUID:85099329; PMID:2981631  
A;Accession: A05267  
A;Molecule type: DNA  
A;Residues: 2504-2576,'E',2578-2611 <WHA2>  
C;Genetics:  
A;Gene: notch; opa  
A;Cross-references: FlyBase:FBgn0004647  
A;Map position: 8.96-9.36  
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3  
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: differentiation; tandem repeat; transmembrane protein  
F;27-43/Domain: transmembrane #status predicted <TMM1>  
F;297-328/Domain: EGF homology <EGX1>  
F;530-561/Domain: EGF homology <EGF1>  
F;568-599/Domain: EGF homology <EGF>  
F;988-1019/Domain: EGF homology <EGX2>  
F;1064-1095/Domain: EGF homology <EGF3>  
F;1187-1218/Domain: EGF homology <EGX3>  
F;1746-1762/Domain: transmembrane #status predicted <TMM2>  
F;1950-1982/Domain: ankyrin repeat homology <AN1>  
F;1983-2015/Domain: ankyrin repeat homology <AN2>  
F;1988-2004/Domain: transmembrane #status predicted <TMM3>  
F;2017-2049/Domain: ankyrin repeat homology <AN3>  
F;2050-2082/Domain: ankyrin repeat homology <AN4>  
F;2083-2115/Domain: ankyrin repeat homology <AN5>  
F;2538-2568/Region: glutamine-rich  
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 18.9%; Score 784.5; DB 1; Length 2703;  
Best Local Similarity 35.2%; Pred. No. 2.5e-39;  
Matches 151; Conservative 52; Mismatches 139; Indels 87; Gaps 10;

QY 167 SQDLHSSGRTDLKYSYRFVDEHYHGGCS-----VFGRPRDRFRGHFTCGERG 215  
Db 608 SNPCHRGKCIDDVNSFKCLCDPGYTGTYICQKQINECESNPCQFDGHCQDRVGSYYC---- 663

QY 216 EKVCNPGWKGOYCTEPI-----CLPGDEQHGFCDKPGECKRCRVGWQGRYC- 261  
Db 664 --QQAGTSGKNCEVNVNECHSNPCNNGATCIDGINSY-----KCQCVPGFTQHCE 713

QY 262 ---DECIRYPGLHGTG---QQPWQCNCQEGWGLFCNQDLNYCTHHKPCKNKNGATCNTG 315  
Db 714 KNVDECISSPCANNVCIDQVNGYKCECPRGFYDAHCLSDVDECASN-PCVNEGRCED-G 771

QY 316 QGSYTCSCRPGYTSSSCEIBEINECDANPCKNKGGSCDTLENSYSCTCPPGFGYGNCELSAM 375  
Db 772 INEFICHCPPPGYTKRCELDIDECSSNPCQHGGTCYDKLNAFSCQCMPGYTGQKCETNID 831  
QY 376 TCADGPCFNGGRCRDNPDG-----G 396  
Db 832 DCVTNPGCGNGGTCTIDKVNKYKCVKVPFTGRDCBSKMDPCASNRCKNEAKCTPSSNFLDF 891  
QY 397 SCRCPLGYSGFNCEKKIDYCS-SSPCANGAQCVDLGNSYICQCQAGFTGRHCDNVDCA 455  
Db 892 SCTCKLGYTRYCDEIDECSLSSPCRNAGASCLNVPGSYRCLCTKGYEGRDCAINTDDCA 951  
QY 456 SFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECA 515  
Db 952 SFPCQNGGTCLDGDYSLCVDFDGHKHCETDINECLSQPCQNGATCSQYVNSYTCTCP 1011  
QY 516 RGYGGLNCQ 524  
Db 1012 LGFSGINCO 1020

RESULT 15  
A49175  
Motch B protein - mouse (fragment)  
N;Alternate names: Notch homolog  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text\_change 16-Aug-2004  
C;Accession: A49175; PH1570; S32113  
R;Lardelli, M.; Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety o  
A;Reference number: A49175; MUID:93178563; PMID:8440332  
A;Accession: A49175  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1203 <LAR>  
A;Cross-references: UNIPROT:O35516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g2879  
A;Experimental source: embryo  
A;Note: sequence extracted from NCBI backbone (NCBIP:126158)  
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.  
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe  
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
F;143-174/Domain: EGF homology <EGX1>  
F;482-513/Domain: EGF homology <EGF1>  
F;560-591/Domain: EGF homology <EGF>  
F;674-705/Domain: EGF homology <EGX2>  
F;712-743/Domain: EGF homology <EGF3>  
F;836-867/Domain: EGF homology <EGX3>

Query Match 18.8%; Score 781; DB 2; Length 1203;  
Best Local Similarity 29.5%; Pred. No. 2e-39;  
Matches 189; Conservative 69; Mismatches 194; Indels 188; Gaps 26;

QY 45 NCCRGGGPGGAGQQQCDCKTFFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSPVDGA 104  
Db 315 NC----QPGTSG---LNCEINFDDCASN-----PCMHGVCVD---GINRYSCVCSP 355

QY 105 G-----GADPAFSNPRI-----FPFGFTWPGTFSLLIEALHTDSPDD 141  
Db 356 GFTGQRNCNIDIDECASNPCRKGATCINDVNGFRICPEGPHHPSCYSQVNECL----- 408

QY 142 LTTENP---ERLISRLATQRHLA----VGEEWSQDLH-----SSGRT--DLKYSYRFV 185  
Db 409 ---SNPCIHGNCTGGLSGYKCLCDAGWVGWVGNCEVDKNECLSNPCQNGGTCNNLVNGYRCT 465

QY 186 CDEHYHGGCSV---FCRPR-----DDRFHFTCGERGEKVCNPGWKGOYCTEPI- 232  
Db 466 CKKGFKGVNCQVNIDECASNPCNLNQCTCFDDVSG-YTCH-----CMLPYTGKNCQTVLA 518

QY 233 -CLPGCDEQHGFC-DKPG---ECKCRVWQGRYC---DECIRYPGLHGTG---QQPW 279  
Db 519 PCSPNPCENAAVCKEAPNFESFSCLCAPGQGRCTVDVDECISKPCMNNGVCHNTQGSY 578

Qy	280	QCNQEGWGGLFCNQDLNYCTHHKPKNGKNGATCTNTGQSYTCSRPGYTGSSCEIEINEC	339
Db	579	VCECPGFGMDCEEDINDCLAN-PCQNGGSCVD-HVNTFSCQCHPGFIGDKCQTDMNEC	636
Qy	340	DANPCKNGGSCDLDLENSYSCTCPPGFYGNKNCELSAMTCADGPCFNGGRCTD-----	390
Db	637	LSEPCNKGGTCSDDYVNSYTCPCAGFHGVHCENNIDECTESSCFNGGTCVDGINSFSLC	696
Qy	391	-----NPD-----GGYSCRCPLGYSGFNCEKKIDYCSSSPCA	422
Db	697	PVGFTGPFCLHDINECSSNPCLNAGTCVDGLGTYRCICPLGYTGKNCQTLVNLCSRSPCK	756
Qy	423	N-----GAQ-----CVDLGNSY	434
Db	757	NKGTGVQEKARPHCLCPPGWDGAYCDVLNVSCAAAALQKGVPEVHLCQHSAGICINAGNTH	816
Qy	435	ICQOAGFTGRHCDNVDDCASPPCVNNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCHEH	494
Db	817	HCQCPGLGYTGSYCEEQLDECASNPCQHGATCNDFIGGYRCECVPGYQGVNCEYEVEDECQN	876
Qy	495	NPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP	534
Db	877	QPCQNGGTCIDLNVNHFKCSCPPGTRGLLCEENIDEACAGP	916

Search completed: November 29, 2004, 13:26:58  
Job time : 22.2447 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 87.6462 Seconds  
(without alignments)  
4779.132 Million cell updates/sec

Title: US-09-783-931-2  
Perfect score: 4153  
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEKDECIATEV 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4153	100.0	728	2	Q90656
2	3495.5	84.2	721	2	Q91902
3	3487.5	84.0	723	1	DL11_HUMAN
4	3449.5	83.1	726	2	Q8AW87
5	3410	82.1	722	2	Q6PFV7
6	3410	82.1	722	2	AAH57400
7	3410	82.1	722	2	AAR30869
8	3410	82.1	722	2	AAH65063
9	3407	82.0	722	1	DL11_MOUSE
10	3354	80.8	714	1	DL11_RAT
11	3064.5	73.8	720	2	Q8UWJ4
12	3061.5	73.7	717	2	P87357
13	2918.5	70.3	772	2	Q6DI48
14	2854.5	68.7	802	2	O57462
15	1945	46.8	642	2	Q7ZXT4
16	1939	46.7	642	2	P79941
17	1925.5	46.4	664	2	Q9IAT6
18	1897	45.7	685	1	DL14_HUMAN
19	1868	45.0	686	1	DL14_MOUSE
20	1863	44.9	686	2	Q9DBU9
21	1852	44.6	615	2	O57409
22	1673	40.3	684	2	Q8I498
23	1560.5	37.6	833	2	Q6T4N0
24	1560.5	37.6	833	2	Q6T4N1
25	1560.5	37.6	833	2	AAR21453
26	1560.5	37.6	833	2	AAR21462
27	1560.5	37.6	833	2	AAR21463
28	1559.5	37.6	833	1	DL_DROME
29	1559.5	37.6	833	2	Q6T4M9
30	1559.5	37.6	833	2	Q6T4N2
31	1559.5	37.6	833	2	Q6T4N3

32	1559.5	37.6	833	2	Q6T4N4	Q6t4n4 drosophila
33	1559.5	37.6	833	2	Q6T4N6	Q6t4n6 drosophila
34	1559.5	37.6	833	2	AAO25024	Aao25024 drosophil
35	1559.5	37.6	833	2	AAR21454	Aar21454 drosophil
36	1559.5	37.6	833	2	AAR21455	Aar21455 drosophil
37	1559.5	37.6	833	2	AAR21456	Aar21456 drosophil
38	1559.5	37.6	833	2	AAR21457	Aar21457 drosophil
39	1559.5	37.6	833	2	AAR21458	Aar21458 drosophil
40	1559.5	37.6	833	2	AAR21459	Aar21459 drosophil
41	1559.5	37.6	833	2	AAR21460	Aar21460 drosophil
42	1559.5	37.6	833	2	AAR21461	Aar21461 drosophil
43	1559.5	37.6	833	2	AAR21464	Aar21464 drosophil
44	1559.5	37.6	833	2	AAR21465	Aar21465 drosophil
45	1559.5	37.6	833	2	AAR21466	Aar21466 drosophil

ALIGNMENTS

RESULT 1

Q90656	PRELIMINARY;	PRT;	728 AA.
AC	Q90656;		
DT	01-NOV-1996 (Tremblrel. 01, Created)		
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	C-Delta-1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Spinal cord;		
RX	MEDLINE=95319507; PubMed=7596411;		
RA	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;		
RT	"Expression of a Delta homologue in prospective neurons in the chick.";		
RL	Nature 375:787-790(1995).		
DR	EMBL; U26590; AAC59689.1; -.		
DR	PIR; I50719; I50719.		
DR	HSP; P00740; LEDM.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0007154; P:cell communication; IEA.		
DR	InterPro; IPR000152; Aax_hydroxyl_s.		
DR	InterPro; IPR001774; DSL.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR001438; EGF_II.		
DR	InterPro; IPR006209; EGF_like.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 6.		
DR	PRINTS; PR00010; EGFLOOD.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00179; EGF_CA; 4.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.		
DR	PROSITE; PS00022; EGF_1; 8.		
DR	PROSITE; PS01186; EGF_2; 8.		
DR	PROSITE; PS50026; EGF_3; 6.		
DR	PROSITE; PS01187; EGF_CA; 2.		
KW	EGF-like domain.		
SQ	SEQUENCE 728 AA; 79861 MW; 93B2D666D2388B7 CRC64;		

Query Match 100.0%; Score 4153; DB 2; Length 728;  
Best Local Similarity 100.0%; Pred. No. 3.6e-268;  
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVWKGLLSNRNCCRGGGPGGAGQQQC 60  
Db 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVWKGLLSNRNCCRGGGPGGAGQQQC 60

Qy 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSPNPIRPFPG 120  
Db 61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSPNPIRPFPG 120  
  
Qy 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKY 180  
Db 121 FTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKY 180  
  
Qy 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
Db 181 SYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQ 240  
  
Qy 241 HGFCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300  
Db 241 HGFCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300  
  
Qy 301 HHKPCKNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCKNGGSCTDLENSYSCT 360  
Db 301 HHKPCKNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCKNGGSCTDLENSYSCT 360  
  
Qy 361 CPFGFYGKNCELSAMTCADGPCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420  
Db 361 CPFGFYGKNCELSAMTCADGPCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420  
  
Qy 421 CANGAQCVDLGNSYICQCQAGTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
Db 421 CANGAQCVDLGNSYICQCQAGTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPGY 480  
  
Qy 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
Db 481 NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540  
  
Qy 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN 600  
Db 541 EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMNN 600  
  
Qy 601 LANQOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRPSVDYNLVHELKNEHSV 660  
Db 601 LANQOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRPSVDYNLVHELKNEHSV 660  
  
Qy 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPSVYSTSKDTKYQSVYVISEEKD 720  
Db 661 KEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPSVYSTSKDTKYQSVYVISEEKD 720  
  
Qy 721 ECIATEV 728  
Db 721 ECIATEV 728

RESULT 2

Q91902  
ID Q91902 PRELIMINARY; PRT; 721 AA.  
AC Q91902;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE X-Delta-1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95319507; PubMed=7596411;  
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;  
RT "Expression of a Delta homologue in prospective neurons in the  
RL chick."; Nature 375:787-790(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95319503; PubMed=7596407;  
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of  
RT the Drosophila neurogenic gene Delta."; Nature 375:761-766(1995).  
RL Nature 375:761-766(1995).  
DR EMBL; L42229; AAC38017.1; -.  
DR HSSP; P00740; 1EDM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000152; Aex hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS00026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW EGF-like domain.  
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;

Query Match 84.2%; Score 3495.5; DB 2; Length 721;  
Best Local Similarity 82.2%; Pred. No. 2.1e-224;  
Matches 600; Conservative 65; Mismatches 54; Indels 11; Gaps 7;

Qy 1 MGRFLLTLALLSALLCRCQVDGSGVFELQLQEFVNKKGLLSNRNCCRGGGPGG-AGQQQ 59  
Db 1 MGQRMLTLLVLSAVL--CQISCSGLFELRLQEFVNKKGLLGNNCCR---PGSLASLQR 55  
  
Qy 60 CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGADPAFSPNPIRPF 119  
Db 56 CECKTFFRICLKHYSNVSPPEPPCTYGGAVTPVLGTNSFVVPE-SSNADPTFSNPIRPF 114  
  
Qy 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLK 179  
Db 115 GFTWPGTFSLLIEALHTADSADDLNTENPERLISRLATORHLTVGEQWSQDLHSSDRTELK 174  
  
Qy 180 YSYRFVCDHEYHYGEGCSVFCRPRDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDE 239  
Db 175 YSYRFVCDHEYHYGEGSDYCRPRDDAFGHFSCGKGKELCNPGWKGLYCTEPICLPGCDE 234  
  
Qy 240 QHGFCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 299  
Db 235 HHGYCDKPGECKCRVWQGRYCDDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 294  
  
Qy 300 THHKPCKNKGATCTNTGQSYTCSRPGYTGSCEIEINECDANPCKNGGSCTDLENSYSC 359  
Db 295 THHKPCENGATCTNTGQSYTCSRPGYTGSNCIEIEVNECDANPCKNGGSCSDLENSYTC 354  
  
Qy 360 TCPPGFYGKNCELSAMTCADGPCFNGGRCRTDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSS 419  
Db 355 SCPPGFYGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCEKKIDYCSSN 414  
  
Qy 420 PCANGAQCVDLGNSYICQCQAGTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479  
Db 415 PCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSPFCQNGGTCQDGINDSYCTCPPG 474  
  
Qy 480 YNGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539  
Db 475 YIGKNCMPITKCEHNPCHNGATCHERNRNVQCARGYGNNCQFLLPE--EKPVVVDL 532  
  
Qy 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIIVCVRLKVQKRHHQPEACRSETETMN 599  
Db 533 TEKYTEGQSGQFPWIAVCAGIVLVLMLLGCAAVVVRVVRVQKRHHQPEACRGSKTMN 592  
  
Qy 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSD-NSDKNGYKVRPSVDYNLVHELKNE 658

Db 593 NLANCQREKDISVFIGTQIKNTNKKIDFLSESNNEKNGYKPRYPVDYNLVHELKNEID 652

QY 659 SVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTKDTKYQSVYVISEE 718

Db 653 SPKEERSKCEAKCSSNDSSEDNVSHSK-RDSSERRRPSAYSSTKDTKYQSVYVISDE 711

QY 719 KDECIATEV 728

Db 712 KDECIATEV 721

RESULT 3

DL11\_HUMAN

ID DL11\_HUMAN STANDARD; PRT; 723 AA.

AC O00548; Q9NU41; Q9UJV2;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)

DE (H-Delta-1) (UNQ146/PRO172).

GN Name=DL11;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99180765; PubMed=10079256;

RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,

RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;

RT "Human ligands of the Notch receptor.";

RL Am. J. Pathol. 154:785-794(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Han W., Ye Q., Moore M.A.S.;

RT "A soluble form of human delta-like-1 inhibits differentiation of

RT hematopoietic progenitor cells.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Oda T., Chandrasekharappa S.C.;

RT "Human Delta 1 gene sequence.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

RN [5]

RP SEQUENCE FROM N.A.

RA Almeida J.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

RP FUNCTION.

RX MEDLINE=21464863; PubMed=11581320;

RA Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,

RA Henrique D., Parreira L.;

RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human

RT lymphoid differentiation.";

RL J. Exp. Med. 194:991-1001(2001).

CC -I- FUNCTION: Acts as a ligand for Notch receptors. Blocks the

CC differentiation of progenitor cells into the B-cell lineage while

CC promoting the emergence of a population of cells with the

CC characteristics of a T-cell/NK-cell precursor.

CC -I- SUBUNIT: Interacts with Notch receptors.

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower

CC expression in brain and muscle and almost no expression in

CC placenta, lung, liver, and kidney.

CC -I- SIMILARITY: Contains 1 DSL domain.

CC -I- SIMILARITY: Contains 8 EGF-like domains.

CC -----

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CC -----

DR EMBL; AF003522; AAB61286.1; -.

DR EMBL; AF196571; AAF05834.1; -.

DR EMBL; AF222310; AAG09716.1; -.

DR EMBL; AY358892; AAQ89251.1; -.

DR EMBL; AL078605; CAB89569.1; -.

DR HSSP; P00740; 1EDM.

DR Genew; HGNC:2908; DLL1.

DR MIM; 606582; -.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005887; C:integral to plasma membrane; NAS.

DR GO; GO:0005112; F:Notch binding; IPI.

DR GO; GO:0030154; P:cell differentiation; TAS.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.

DR GO; GO:0009912; P:hair cell fate commitment; ISS.

DR GO; GO:0030097; P:hemopoiesis; NAS.

DR GO; GO:0042472; P:inner ear morphogenesis; ISS.

DR GO; GO:0007399; P:neurogenesis; ISS.

DR GO; GO:0007219; P:Notch signaling pathway; NAS.

DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.

DR GO; GO:0030155; P:regulation of cell adhesion; TAS.

DR InterPro; IPR000152; Asx\_hydroxyl\_s.

DR InterPro; IPR001774; DSL.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001438; EGF\_II.

DR InterPro; IPR006209; EGF\_like.

DR Pfam; PF01414; DSL; 1.

DR Pfam; PF00008; EGF; 6.

DR PRINTS; PR00010; EGFBL00D.

DR SMART; SM00051; DSL; 1.

DR SMART; SM00179; EGF\_CA; 4.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.

DR PROSITE; PS00022; EGF\_1; 8.

DR PROSITE; PS01186; EGF\_2; 8.

DR PROSITE; PS00026; EGF\_3; 7.

DR PROSITE; PS01187; EGF\_CA; 1.

KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;

KW Repeat; Signal; Transmembrane.

FT SIGNAL 1 17 Potential.

FT CHAIN 18 723 Delta-like protein 1.

FT DOMAIN 18 545 Extracellular (Potential).

FT TRANSMEM 546 568 Potential.

FT DOMAIN 569 723 Cytoplasmic (Potential).

FT DOMAIN 159 221 DSL.

FT DOMAIN 226 254 EGF-like 1.

FT DOMAIN 257 285 EGF-like 2.

FT DOMAIN 292 325 EGF-like 3.

FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).

FT DOMAIN 370 402 EGF-like 5.

FT DOMAIN 409 440 EGF-like 6.

FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).

FT DOMAIN 485 516 EGF-like 8.

FT DISULFID 226 237 By similarity.

FT DISULFID 230 243 By similarity.

FT	DISULFID	245	254	By similarity.	
FT	DISULFID	257	268	By similarity.	
FT	DISULFID	263	274	By similarity.	
FT	DISULFID	276	285	By similarity.	
FT	DISULFID	292	304	By similarity.	
FT	DISULFID	298	314	By similarity.	
FT	DISULFID	316	325	By similarity.	
FT	DISULFID	332	343	By similarity.	
FT	DISULFID	337	352	By similarity.	
FT	DISULFID	354	363	By similarity.	
FT	DISULFID	370	381	By similarity.	
FT	DISULFID	375	391	By similarity.	
FT	DISULFID	393	402	By similarity.	
FT	DISULFID	409	420	By similarity.	
FT	DISULFID	414	429	By similarity.	
FT	DISULFID	431	440	By similarity.	
FT	DISULFID	447	467	By similarity.	
FT	DISULFID	469	478	By similarity.	
FT	DISULFID	485	496	By similarity.	
FT	DISULFID	490	505	By similarity.	
FT	DISULFID	507	516	By similarity.	
FT	CARBOHYD	477	477	N-linked (GlcNAc. . .) (Potential).	
FT	CONFLICT	498	498	E -> Q (in Ref. 2).	
FT	CONFLICT	502	502	G -> R (in Ref. 4 and 5).	
FT	CONFLICT	510	510	G -> S (in Ref. 2).	
SQ	SEQUENCE	723 AA;	77956 MW;	B4EC455FFA32A12B CRC64;	
Query Match 84.0%; Score 3487.5; DB 1; Length 723;					
Best Local Similarity 83.2%; Pred. No. 7.3e-224;					
Matches 608; Conservative 47; Mismatches 65; Indels 11; Gaps 7;					
Qy	1	MGGRELLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQC	60		
Dd	1	MGRCALALAVLSALL--CQWSSGVSFELKLQEFVNKKGLLGNRNCCR----	GGAGPPPC	54	
Qy	61	DKTFFRVCLKHYQASVSPEPPCTYGSATIPVLGANSFSVPDGGAGGADPAFSPNIRPPFG	120		
Dd	55	ACRTFFRVCLKHYQASVSPEPPCTYGSATIPVLGVDSFSLPDG--GGADSAFSPNIRPPFG	113		
Qy	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRTDLKY	180		
Dd	114	FTWPGTFSLIIEALHTDSPDDLATENPERLISRATQRHLTVGEEWSQDLHSSGRTDLKY	173		
Qy	181	SYRFVCDHEHYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGYCTEPICLPQCDEQ	240		
Dd	174	SYRFVCDHEHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPQCDEQ	233		
Qy	241	HGFCDKPGECKCRVGWQGRYCDICIRYPGLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT	300		
Dd	234	HGFCDKPGECKCRVGWQGRYCDICIRYPGLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT	293		
Qy	301	HHKPCKNGATCTNTGQGSYTCSCRPGYTGSCEIEINECDANPCKNNGSCSTDLENSYSCT	360		
Dd	294	HHKPCKNGATCTNTGQGSYTCSCRPGYTGCCELGIDECDFSPCKNGGSCSTDLENSYSCT	353		
Qy	361	CPPGFYCKNCELSAMTCADGPCFNGGRCTDNPDDGGYSRCPLGYSGFNCCKIDYCSSSP	420		
Dd	354	CPPGFYCKICELSAMTCADGPCFNGGRCSDSPDGGYSRCRCPVGYSGFNCCKIDYCSSSP	413		
Qy	421	CANGAQCVDLGNYSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGY	480		
Dd	414	CSNGAKCVDLGDAYLCRCQAQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPPGY	473		
Qy	481	NGKNCSTPVSRCENHPCHNGATCHERSNRYVCECARGYGILNCQFLLPEPPQGPVIVDFT	540		
Dd	474	TGRNCAPVSRCEHAPCHNGATCHERGHGVCECARGYGGNCQFLLPELPGPVAVDLT	533		
Qy	541	EKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVVCRLVKVQRHHQPEACRSETETMNN	600		
Dd	534	EK-LEGQGGPPWAVACGAVILVLMLLGCAAIVVVCRLVRLQHRPPADPCRGETETMNN	592		
Qy	601	LANCQREKDISIVIGATQIKNTNKKVDVDFHSDNS--DKNGYKVRYPVSDYNLVHELKNE	658		
Query Match 83.1%; Score 3449.5; DB 2; Length 726;					
Best Local Similarity 83.2%; Pred. No. 2.5e-221;					
Matches 603; Conservative 46; Mismatches 69; Indels 7; Gaps 5;					
Qy	8	TLALLSALLC-RCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQ-QQCDCKTF	65		
Dd	5	SLLACAAALLCVLCQVCSGVSFELKLQEFVNKKGLNANCCRAGGSVQQGALLQCQCRTF	64		
Qy	66	FRVCLKHYQASVSPEPPCTYGSATIPVLGANSFSVPDGGAGADPAFSPNIRFPFGFTWPG	125		
Dd	65	FRVCLKHYQANVSPEPPCTYGSATIPVLGQGSFTVPE--GGEATFSNPIRIAFGFTWPG	121		
Qy	126	TFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEEWSQDLHSSGRTDLKYSYRFPV	185		
Dd	122	TFSLIIGALHTDSPDDLSTENPDRLISRMAIQRHLAVGEDWSQDSQSSGRTDLKYSYRFPV	181		
Qy	186	CDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQHGFC	245		



Db 182 CDEHYYGECVSFCRPRDDTFGHFTCGERGEKQCNOGWKGQYCTEAICLPLGCDQHGFC D 241

QY 246 KPGECKCRVWGQGRYCDECIRYPGCLHGTCCQWPQNCQEGWGGLFCNQDLNYCTHHKPC 305

Db 242 RPGECKCRVWGQGRYCDECIRYPGCLHGTCCQWPQNCQEGWGGLFCNQDLNYCTHHKPC 301

QY 306 KNGATCTNTGQGSYTCSCRPGYTGSCEIEINECDANPCKNKGSCDLDENSYSCTCPPGF 365

Db 302 KNAATCTNTGQGSYTCSCRPGYTGANCEIEVNECEASPCKNKGSCADLENSYSCSPPGF 361

QY 366 YGKNCELSAMTCADGPCFNGGRCTDNPDDGYSRCPLGYSGFNCEKKIDYCSSSPCANGA 425

Db 362 YGKNCELSAMTCADGPCFNGGRCDNPEGGYSCRCPLSYSGFNCEKKIDYCSSNPGSNGA 421

QY 426 QCVDLGNYSYICQCQAGFTGRHCDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGNGKNC 485

Db 422 HCVDLGNYSYICQCLDGFSGRHCDNLDDCASYPCANGGTCQDGVNDYSCTCPPGNGKNC 481

QY 486 STPVSRCENHPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPPQGPVIVDFTKEYTE 545

Db 482 STPVSRCESHPCHNGATCHERNRYVCECARGYGGLNCQFLPPEQPEHDTGDNTEKEYTE 541

QY 546 QONSQFPWIAVCAGIILVLMLLGCAIIVCVRLKVQK-RHHQPEACRSETETMNNLANC 604

Db 542 DQGGQFPWIAVCAGIILVLMLLFGCAAVVFCFLKMHKQRQSDSYRGESETMNNLANC 601

QY 605 QREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPSVDYNLVHELKNEDSVKEE 663

Db 602 RREKDISVSVIGATQIKNTNKKADLYSESTDKNYKARYPSVDYNLVHELKHEDSVKEE 661

QY 664 HGKCEAKCETYDSEAEKSAVOLKSSDTSERKRPSVYSTSKDTKYQSVYVISEEKDECI 723

Db 662 HGKRESKCIANGSEADEKHPVLQKSSETSERRRPESLYSTSKETKYQSVYVISEAKDECI 721

QY 724 IATEV 728

Db 722 IATEV 726

RESULT 5

Q6PFV7

ID Q6PFV7 PRELIMINARY; PRT; 722 AA.

AC Q6PFV7;

DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 01-OCT-2004 (TReMBLrel. 28, Last annotation update)

DE Delta-like 1.

GN Name=Dll1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Mouse;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywineki M.I., Skolaka U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Mouse;

RA Strausberg R.;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Mouse;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Nagaraja R., Waeltz P., Brathwaite M.E.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBBJ databases.

CC -1- SIMILARITY: Contains 8 EGF-like domains.

DR EMBL; BC057400; AAH57400.1; -.

DR EMBL; BC065063; AAH65063.1; -.

DR EMBL; AY497019; AAR30869.1; -.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007386; P:compartment specification; IMP.

DR GO; GO:0007368; P:determination of left/right symmetry; IMP.

DR GO; GO:0001757; P:somite specification; IMP.

DR InterPro; IPR000152; Asx hydroxyl\_S.

DR InterPro; IPR001774; DSL.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001438; EGF\_II.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.

DR Pfam; PF01414; DSL; 1.

DR Pfam; PF00008; EGF; 6.

DR Pfam; PF07645; EGF\_CA; 1.

DR PRINTS; PR00010; EGFBL00D.

DR SMART; SM00051; DSL; 1.

DR SMART; SM00181; EGF; 8.

DR SMART; SM00179; EGF\_CA; 6.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.

DR PROSITE; PS00022; EGF\_1; 8.

DR PROSITE; PS01186; EGF\_2; 8.

DR PROSITE; PS50026; EGF\_3; 6.

DR PROSITE; PS01187; EGF\_CA; 2.

KW EGF-like domain.

SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7BEC75E CRC64;

Query Match 82.1%; Score 3410; DB 2; Length 722;

Best Local Similarity 79.5%; Pred. No. 1.1e-218;

Matches 581; Conservative 72; Mismatches 66; Indels 12; Gaps 6;

QY 1 MGGRFLTLTALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGQQQ 59

Db 1 MGRRSALALAVVSALL--CQWSSSGVFELKLQEFVNKKGLLGNRNCCRGSGP-----P 52

QY 60 CDCKTFFRVCLKHQASVSPEPPCTYGSAITPVLGANSFSVPDAGGADPAFSPNPIRFPF 119

Db 53 CACRTFFRVCLKHQASVSPEPPCTYGSATPVLGVDSFSLPDGA-GIDPAFSPNPIRFPF 111

QY 120 GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLK 179

Db 112 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLR 171

QY 180 YSYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKGOYCTEPICLPGCDE 239

Db 172 YSYRFVCDHYHYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDD 231

QY 240 QHGFCDKPGECKCRVWGQGRYDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 299  
|||:|||||  
Db 232 QHGYCDKPGECKCRVWGQGRYDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 291  
|||:|||||  
QY 300 THHKPCXGATCTNTGQSGYTSCRPYGTGSSCEIEINECDANPCXNGGSCDTLENSYSC 359  
|||||:|||||  
Db 292 THHKPCXGATCTNTGQSGYTSCRPYGTGANCELEVECAPSPCKNGASCTDLEDSFSC 351  
|||||:|||||  
QY 360 TCPPGFYGNCELSAMTCADGPCFNGGRCTDNPDGYSRCPLGYSGFNCCKIDYCSSS 419  
|||||:|||||  
Db 352 TCPPGFYGNCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCCKMDLCSGSS 411  
|||||:|||||  
QY 420 PCANGAQCVDLGNYSYCQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479  
|||:|||||  
Db 412 PCSNGAKCVDLGNYSYLCRCQAGSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471  
|||||:|||||  
QY 480 YNGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPIVDF 539  
| |||:|||||  
Db 472 YTGKNCAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNCFLLPEPPPGPMVVDL 531  
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QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQRHHQPEACRSETMTN 599  
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Db 532 SERHMSGGPPFWAVCAGVVLVLLLLGCAAVVCVRLKLQKHQPPPEPCGGGETMTN 591  
|||||:|||||  
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSDN -SDKNGYKVRYPVSDYNLVHELK-NE 657  
|||||:|||||  
Db 592 NLANCQREKDVSVIIIGATQIKNTNKKADFHGDHGAESFKVRYPTVDYNLVRDLKGDE 651  
|||||:|||||  
QY 658 DSVKEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRDPDSYSTKDTKYQSVYVISE 717  
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Db 652 ATVRDTHSKRDTKCQSSSAGEEKIAPTLRGGEIPDRKPESVYSTKDTKYQSVYVLSA 711  
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QY 718 EKDECIIATEV 728  
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Db 712 EKDECVIATEV 722  
|||||:|||||

RESULT 6

AAH57400  
ID AAH57400 PRELIMINARY; PRT; 722 AA.  
AC AAH57400;  
DT 02-MAR-2004 (TremBLrel. 27, Created)  
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)  
DE Delta-like 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057400; AAH57400.1; -.  
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;  
  
Query Match 82.1%; Score 3410; DB 2; Length 722;  
Best Local Similarity 79.5%; Pred. No. 1.1e-218;  
Matches 581; Conservative 72; Mismatches 66; Indels 12; Gaps 6;  
  
QY 1 MGRFLLTLALLSALLCRCQVDGSGVFELKQEFVKNKGLLSNRNCCRGG-GPGGAGQQQ 59  
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Db 1 MGRSALALAVVSALL--CQWSSGVFELKQEFVKNKGLLGNRNCCRGSGP-----P 52  
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QY 60 CDCKTFFRVCLKHYQASVSPPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSPNIRPFF 119  
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Db 53 CACRTFFRVCLKHYQASVSPPEPPCTYGSATPVLGVDSFSLPDGA-GIDPAFSPNIRPFF 111  
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QY 120 GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLK 179  
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Db 112 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTQRHLTVGEWSQDLHSSGRTDLR 171  
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QY 180 YSYRFVCDHYHYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDE 239  
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Db 172 YSYRFVCDHYHYGEGCSVFCRPRDDAFHFTCGRGEKMCDFGWKQYCTDPICLPGCDD 231  
|||:|||||  
QY 240 QHGFCDKPGECKCRVWGQGRYDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 299  
|||||:|||||  
Db 232 QHGYCDKPGECKCRVWGQGRYDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 291  
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QY 300 THHKPCXGATCTNTGQSGYTSCRPYGTGSSCEIEINECDANPCXNGGSCDTLENSYSC 359  
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Db 292 THHKPCXGATCTNTGQSGYTSCRPYGTGANCELEVECAPSPCKNGASCTDLEDSFSC 351  
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QY 360 TCPPGFYGNCELSAMTCADGPCFNGGRCTDNPDGYSRCPLGYSGFNCCKIDYCSSS 419  
|||||:|||||  
Db 352 TCPPGFYGNCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCCKMDLCSGSS 411  
|||||:|||||  
QY 420 PCANGAQCVDLGNYSYCQAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479  
|||:|||||  
Db 412 PCSNGAKCVDLGNYSYLCRCQAGSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471  
|||||:|||||  
QY 480 YNGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPIVDF 539  
| |||:|||||  
Db 472 YTGKNCAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNCFLLPEPPPGPMVVDL 531  
|||:|||||  
QY 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQRHHQPEACRSETMTN 599  
: |||:|||||  
Db 532 SERHMSGGPPFWAVCAGVVLVLLLLGCAAVVCVRLKLQKHQPPPEPCGGGETMTN 591  
|||||:|||||  
QY 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSDN -SDKNGYKVRYPVSDYNLVHELK-NE 657  
|||||:|||||  
Db 592 NLANCQREKDVSVIIIGATQIKNTNKKADFHGDHGAESFKVRYPTVDYNLVRDLKGDE 651  
|||||:|||||  
QY 658 DSVKEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRDPDSYSTKDTKYQSVYVISE 717  
: |||:|||||  
Db 652 ATVRDTHSKRDTKCQSSSAGEEKIAPTLRGGEIPDRKPESVYSTKDTKYQSVYVLSA 711  
|||||:|||||  
QY 718 EKDECIIATEV 728  
|||||:|||||  
Db 712 EKDECVIATEV 722  
|||||:|||||

RESULT 7

AAR30869  
ID AAR30869 PRELIMINARY; PRT; 722 AA.  
AC AAR30869;  
DT 02-MAR-2004 (TremBLrel. 27, Created)  
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)  
DE Delta like-1.





Db 292 THHKPCRNATCTNTQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSC 351  
Qy 360 TCPPEFGKNCELSAMTCADGPGCFNGGRCTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSS 419  
Db 352 TCPPEFGKVCELSAMTCADGPGCFNGGRCSNDPDGGYTCHCPLGFSGFNCCKMDLCSSS 411  
Qy 420 PCANGAQCVDLGNYSYCQCAGFTGRHCDNDVDDCASFPVCVNGGTCQDGVNDYSCTCPPG 479  
Db 412 PCSNGAKCVDLGNYSYLCRCQAGESGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG 471  
Qy 480 YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPQGPIVDF 539  
Db 472 YTGKNCAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL 531  
Qy 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMN 599  
Db 532 SERHMSQGGPFPWAVACGVVLLVLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMN 591  
Qy 600 NLANCOREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPVSDYNLVHELK-NE 657  
Db 592 NLANCOREKDVSVIIGATQIKNTNKKADFGHDGHAESFKVRYPTVDYNLVRLDKGDE 651  
Qy 658 DSVKEEHGKCEAKCETYDSEAEKSAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVVISE 717  
Db 652 ATVRDTHSKRDTKQCSQSSAGEEKIAPTLRGGEIPDRKRPEVYSTSKDTKYQSVVLSA 711  
Qy 718 EKDECIIATEV 728  
Db 712 EKDECVIATEV 722

RESULT 9

DL11\_MOUSE STANDARD; PRT; 722 AA.  
AC Q61483;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).  
GN Name=Dl11;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;  
RX MEDLINE=95401858; PubMed=7671806;  
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;  
RT "Transient and restricted expression during mouse embryogenesis of  
RT Dl11, a murine gene closely related to Drosophila Delta.";  
RL Development 121:2407-2418(1995).  
CC -!- FUNCTION: May be involved in cell-to-cell communication in  
CC mammalian embryos. May have a role in cellular interactions  
CC underlying somitogenesis and development of the nervous system.  
CC -!- SUBUNIT: Interacts with Notch receptors.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial  
CC mesoderm and nervous system. Expressed at high levels in adult  
CC heart and at lower levels, in adult lung.  
CC -!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.  
CC Expression then decreases and increases again in the adult.  
CC -!- SIMILARITY: Contains 1 DSL domain.  
CC -!- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X80903; CAA56865.1; -.  
DR PIR; I48324; I48324.  
DR HSSP; P00740; 1EDM.  
DR IntAct; Q61483; -.  
DR MGD; MGI:104659; Dl11.  
DR GO; GO:0005576; C:extracellular; ISS.  
DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
DR GO; GO:0005112; F:Notch binding; IPI.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001709; P:cell fate determination; ISS.  
DR GO; GO:0007386; P:compartment specification; IMP.  
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.  
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.  
DR GO; GO:0009912; P:hair cell fate commitment; NAS.  
DR GO; GO:0030097; P:hemopoiesis; ISS.  
DR GO; GO:0042472; P:inner ear morphogenesis; NAS.  
DR GO; GO:0007399; P:neurogenesis; NAS.  
DR GO; GO:0007219; P:Notch signaling pathway; ISS.  
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); NAS.  
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBL00D.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 7.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
KW Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 722 Delta-like protein 1.  
FT DOMAIN 18 545 Extracellular (Potential).  
FT TRANSMEM 546 568 Potential.  
FT DOMAIN 569 722 Cytoplasmic (Potential).  
FT DOMAIN 158 220 DSL.  
FT DOMAIN 225 253 EGF-like 1.  
FT DOMAIN 256 284 EGF-like 2.  
FT DOMAIN 291 324 EGF-like 3.  
FT DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).  
FT DOMAIN 369 401 EGF-like 5.  
FT DOMAIN 408 439 EGF-like 6.  
FT DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).  
FT DOMAIN 484 515 EGF-like 8.  
FT DISULFID 225 236 By similarity.  
FT DISULFID 229 242 By similarity.  
FT DISULFID 244 253 By similarity.  
FT DISULFID 256 267 By similarity.  
FT DISULFID 262 273 By similarity.  
FT DISULFID 275 284 By similarity.  
FT DISULFID 291 303 By similarity.  
FT DISULFID 297 313 By similarity.  
FT DISULFID 315 324 By similarity.  
FT DISULFID 331 342 By similarity.  
FT DISULFID 336 351 By similarity.  
FT DISULFID 353 362 By similarity.  
FT DISULFID 369 380 By similarity.  
FT DISULFID 374 390 By similarity.  
FT DISULFID 392 401 By similarity.  
FT DISULFID 408 419 By similarity.  
FT DISULFID 413 428 By similarity.  
FT DISULFID 430 439 By similarity.  
FT DISULFID 446 466 By similarity.  
FT DISULFID 468 477 By similarity.  
FT DISULFID 484 495 By similarity.  
FT DISULFID 489 504 By similarity.  
FT DISULFID 506 515 By similarity.



FT	CARBOHYD	476	476	N-linked (GlcNAc...)	(Potential).
SQ	SEQUENCE	722	AA; 78448 MW; 95F581B56DCEC9B0	CRC64;	
Query Match					
Best Local Similarity 79.5%; Pred. No. 1.7e-218;					
Matches 581; Conservative 71; Mismatches 67; Indels 12; Gaps 6;					
Qy	1	MGRFLLTLALLSALLCRQVDGSGVFELKQEFVNKKGLLSNRNCCRG	G-GPGAGQQQ	59	
Db	1	MGRSALALAVVSALL--CQWSSGVFELKQEFVNKKGLLSNRNCCRG	SGP-----P	52	
Qy	60	CDCKTFRVCLKHQYASVSPPEPCTYGSATPVLGANSFVDPD	GAGDPAFNP	119	
Db	53	CACRTFRVCLKHQYASVSPPEPCTYGSATPVLGVDSFSLPDGA	-GIDPAFNP	111	
Qy	120	GFTWPGTFSLLIEALHTDSPDDLTENPERLISRLATQRHLAVGE	WSQDLHSSGR	179	
Db	112	GFTWPGTFSLLIEALHTDSPDDLTENPERLISRLTQRHLTVGE	WSQDLHSSGR	171	
Qy	180	YSYRFVCDHYHGGCVFCRPRDDRFHFTCGERGEKVCNPGWK	GQYCTEPICLPGCDE	239	
Db	172	YSYRFVCDHYHGGCVFCRPRDDAFGHFTCGERGEKMDPGWK	GQYCTDPICLPGCDD	231	
Qy	240	QHGFCDKPGECKRVRGQGRYCDCEIRYPGLHGTQOQPWQCNC	QEGWGLFCNQDLYNC	299	
Db	232	QHGYCDKPGECKRVRGQGRYCDCEIRYPGLHGTQOQPWQCNC	QEGWGLFCNQDLYNC	291	
Qy	300	THHKPCNGATCTNTGQSYTCSRPYTGSSCEIENECDANPC	NGSGSCTDLENSYSC	359	
Db	292	THHKPCNGATCTNTGQSYTCSRPYTGANCELEVEDECAP	SPCKNGASCTDLEDSFSC	351	
Qy	360	TCPPGFYGNKCELSAMTCADGPCFNGGRCRTDNP	DGYSYCRCLGYSGFNCEKKIDYCSSS	419	
Db	352	TCPPGFYGNKCELSAMTCADGPCFNGGRCSDNP	DGYSYCRCLGYSGFNCEKKMDLCSSS	411	
Qy	420	PCANGAQCVDLGNSYICQAGFTGRHCDNDVDDCASFP	CVNGGTCQDGVNDYSCTCPPG	479	
Db	412	PCNAGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSP	CANGGTCRDSVNDFSCTCPPG	471	
Qy	480	YNGKNCSTPVSRCHEHNPCHNGATCHERSNRYVCECARG	YVGLNCQFLLPPEPQGPVIVDF	539	
Db	472	YTGKNCAPVSRCEHAPCHNGATCHORQRYMCECAQY	GGPNQCFLLPEPPGPMVVDL	531	
Qy	540	TEKYTEGQNSQFPWIAVCAGIILVLLMLLGC	AAIVCVRLKVQKRHHQPEACRSETETMN	599	
Db	532	SERHMESQGGPFPWVAVCAGVVLVLLMLLGC	AAVVCVRLKLQKHQPPPEPCGETETMN	591	
Qy	600	NLANCQREKDISVIGATQIKNTNKKVDFHSDN	-SDKNGYKVRYPSPVDYNLVHELK-NE	657	
Db	592	NLANCQREKDVSVIIGATQIKNTNKKADFHGDGAKKSS	FKVRYPTVDYNLVRLDLKGDE	651	
Qy	658	DSVKEEHGKCEAKCETYDSEAEKSAVOLKSSDTS	ERKRPDSVYSTSKDTKYQSVYVISE	717	
Db	652	ATVRDTHSKRDTKCQSSSAGEEKIAPT	LRGGEIPDRKRPEVYSTSKDTKYQSVYVLSA	711	
Qy	718	EKDECIATEV	728		
Db	712	EKDECVIATEV	722		
RESULT 10					
DL11_RAT					
ID	DL11_RAT	STANDARD;	PRT;	714	AA.
AC	P97677;				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).				
GN	Name=D11;				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				

RN	[1]	SEQUENCE FROM N.A.
RP	Disibio G., Hebshi L., Boulter J., Weinmaster G.;	
RA	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.	
RL	-!- FUNCTION: May be involved in cell-to-cell communication in	
CC	mammalian embryos. May have a role in cellular interactions	
CC	underlying somitogenesis and development of the nervous system (By	
CC	similarity).	
CC	-!- SUBUNIT: Interacts with Notch receptors.	
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-!- SIMILARITY: Contains 1 DSL domain.	
CC	-!- SIMILARITY: Contains 8 EGF-like domains.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; U78889; AAB37343.1; -.	
DR	HSP; P08709; IBF9.	
DR	RGD; 70949; D111.	
DR	GO; GO:0005576; C:extracellular; ISS.	
DR	GO; GO:0005887; C:integral to plasma membrane; ISS.	
DR	GO; GO:0005112; F:Notch binding; IPI.	
DR	GO; GO:0030154; P:cell differentiation; ISS.	
DR	GO; GO:0001709; P:cell fate determination; ISS.	
DR	GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.	
DR	GO; GO:0009912; P:hair cell fate commitment; NAS.	
DR	GO; GO:0030097; P:hemopoiesis; ISS.	
DR	GO; GO:0042472; P:inner ear morphogenesis; ISS.	
DR	GO; GO:0007399; P:neurogenesis; NAS.	
DR	GO; GO:0007219; P:Notch signaling pathway; NAS.	
DR	GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.	
DR	GO; GO:0030155; P:regulation of cell adhesion; ISS.	
DR	InterPro; IPR000152; Asx_hydroxyl_s.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR006209; EGF_like.	
DR	Pfam; PF01414; DSL; 1.	
DR	Pfam; PF00008; EGF; 6.	
DR	PRINTS; PR00010; EGFLOOD.	
DR	SMART; SM00051; DSL; 1.	
DR	SMART; SM00179; EGF_CA; 4.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.	
DR	PROSITE; PS00022; EGF_1; 8.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS50026; EGF_3; 7.	
DR	PROSITE; PS01187; EGF_CA; 2.	
KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein;	
KW	Repeat; Signal; Transmembrane.	
FT	SIGNAL	1 17 Potential.
FT	CHAIN	18 714 Delta-like protein 1.
FT	DOMAIN	18 537 Extracellular (Potential).
FT	TRANSMEM	538 560 Potential.
FT	DOMAIN	561 714 Cytoplasmic (Potential).
FT	DOMAIN	158 220 DSL.
FT	DOMAIN	225 253 EGF-like 1.
FT	DOMAIN	256 284 EGF-like 2.
FT	DOMAIN	291 324 EGF-like 3.
FT	DOMAIN	331 362 EGF-like 4, calcium-binding (Potential).
FT	DOMAIN	369 401 EGF-like 5.
FT	DOMAIN	408 439 EGF-like 6.
FT	DOMAIN	446 477 EGF-like 7, calcium-binding (Potential).
FT	DOMAIN	484 515 EGF-like 8.
FT	DISULFID	225 236 By similarity.
FT	DISULFID	229 242 By similarity.
FT	DISULFID	244 253 By similarity.
FT	DISULFID	256 267 By similarity.

FT	DISULFID	262	273	By similarity.
FT	DISULFID	275	284	By similarity.
FT	DISULFID	291	303	By similarity.
FT	DISULFID	297	313	By similarity.
FT	DISULFID	315	324	By similarity.
FT	DISULFID	331	342	By similarity.
FT	DISULFID	336	351	By similarity.
FT	DISULFID	353	362	By similarity.
FT	DISULFID	369	380	By similarity.
FT	DISULFID	374	390	By similarity.
FT	DISULFID	392	401	By similarity.
FT	DISULFID	408	419	By similarity.
FT	DISULFID	413	428	By similarity.
FT	DISULFID	430	439	By similarity.
FT	DISULFID	446	466	By similarity.
FT	DISULFID	468	477	By similarity.
FT	DISULFID	484	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	515	By similarity.
FT	CARBOHYD	476	476	N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE	714 AA;	77378 MW;	4B8EE2272BAEA27E CRC64;
Query Match 80.8%; Score 3354; DB 1; Length 714;				
Best Local Similarity 78.4%; Pred. No. 5.6e-215;				
Matches 573; Conservative 69; Mismatches 69; Indels 20; Gaps 7;				
Qy	1	MGRFLTLTALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGQQQ	59	
Dd	1	MGRSALALAVVSALL--CQVSSGVSFELKLQEFVNKKGLLSNRNCCRGSGGP-----P	52	
Qy	60	CDCKTFFRVCLKHYYQASVSPPEPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF	119	
Dd	53	CACRTFFRVCLKHYYQASVSPPEPCTYGSAVTAVLGVDVSFLPDGA-GIDPAFSNPIRFPF	111	
Qy	120	GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRATQRHLAVGEWSQDLHSSGRDCLK	179	
Dd	112	GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRDCLR	171	
Qy	180	YSYRFVCDHHYYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDE	239	
Dd	172	YSYRFVCDHHYYGEGCSVFCRPRDDAFGHFTCGERGEKMDPGWKQGYCTDPICLPGCDD	231	
Qy	240	QHGFCDKPGECKRVGWQGRYCDDECIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYC	299	
Dd	232	QHGYCDKPGECKRVGWQGRYCDDECIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYC	291	
Qy	300	THHKPCKNKNGATCTNTQGSGYTCSCRPGYTGSSCEIIEINCDANPCKNGGSCDTLENSYSC	359	
Dd	292	THHKPCRNKNGATCTNTQGSGYTCSCRPGYTGANCELEVDCAFPSCRNGGSCDTLEDSYSC	351	
Qy	360	TCPPGYGKNCELSAMTCADGPGFNGGRCTDNDPDGGYSCRCPLGYSGFNCEKKIDYCSSS	419	
Dd	352	TCPPGYGKVCELSAMTCADGPGFNGGRCSNDPDGGYTCCHPAGFSGFNCEKKIDLCSSS	411	
Qy	420	PCANGAQCVDLGNYSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCCQGVNDYSCTCPPG	479	
Dd	412	PCSNAGKACVDLGNYSYLCRCQTFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG	471	
Qy	480	YNGKNCSTPVSRCHEHNPCHNGATCHEHSNRYYVCECARGYGGLNCQFLLPEPPQGPVIVDF	539	
Dd	472	YTGNC SAPVSRCEHAPCHNGATCHQGRQRYMCECAQYGGANCQFLLPEPPPDLLIVA--	529	
Qy	540	TEKYTEGQNSQFPWIAVCAGIILVMLLLGCAAIVVCVRLKVKQRHHQPEACRSETETMN	599	
Dd	530	-----AQGGSFPWAVACGVVVLVLLLLLGCAAVVVCVRLKLQKHQPPDPCCGETETMN	583	
Qy	600	NLANCQREKDISISVIGATQIKNTNKKVDVFDHSDN-SDKNGYKVRYPVSDYNLVHELK-NE	657	
Dd	584	NLANCQREKDVSVIIIGATQIKNTNKKADFHGDHGDADSKSSFKARYPTVDYNLIRDLKGDE	643	
Qy	658	DSVKEBHGKCEAKCETYDSEABEKS AVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE	717	
Dd	644	ATVRDAHSKRDTKCQSQGSVGBEKSSTSLRGGEVDPDRKPESVYSTSKDTKYQSVYVLSA	703	

Qy	718	EKDECIATEV	728	
Dd	704	EKDECVIATEV	714	
RESULT 11				
Q8UWJ4	ID	Q8UWJ4	PRELIMINARY;	PRT; 720 AA.
AC	Q8UWJ4;			
DT	01-MAR-2002	(Tremblrel. 20, Created)		
DT	01-MAR-2002	(Tremblrel. 20, Last sequence update)		
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)		
DE	DeltaD protein.			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22248969; PubMed=12361969;			
RA	Hans S., Campos-Ortega J.A.;			
RT	"On the organisation of the regulatory region of the zebrafish deltaD			
RT	gene.";			
RL	Development 129:4773-4784(2002).			
DR	EMBL;	AF426384;	AAL31528.1;	-.
DR	HSSP;	P00740;	1EDM.	
DR	GO;	GO:0016020;	C:membrane;	IEA.
DR	GO;	GO:0005509;	F:calcium ion binding;	IEA.
DR	GO;	GO:0007154;	P:cell communication;	IEA.
DR	InterPro;	IPR000152;	Asx_hydroxyl_S.	
DR	InterPro;	IPR001774;	DSL.	
DR	InterPro;	IPR000742;	EGF_2.	
DR	InterPro;	IPR001881;	EGF_Ca.	
DR	InterPro;	IPR001438;	EGF_II.	
DR	InterPro;	IPR006209;	EGF_like.	
DR	Pfam;	PF01414;	DSL;	1.
DR	Pfam;	PF00008;	EGF;	6.
DR	PRINTS;	PR00010;	EGFBLOOD.	
DR	SMART;	SM00051;	DSL;	1.
DR	SMART;	SM00179;	EGF_CA;	4.
DR	PROSITE;	PS00010;	ASX_HYDROXYL;	3.
DR	PROSITE;	PS00022;	EGF_1;	8.
DR	PROSITE;	PS01186;	EGF_2;	8.
DR	PROSITE;	PS00026;	EGF_3;	6.
DR	PROSITE;	PS01187;	EGF_CA;	2.
KW	EGF-like domain.			
SQ	SEQUENCE	720 AA;	79380 MW;	DE6B7393E2AA0FE6 CRC64;

Query Match 73.8%; Score 3064.5; DB 2; Length 720;  
Best Local Similarity 73.3%; Pred. No. 1.1e-195;  
Matches 531; Conservative 81; Mismatches 95; Indels 17; Gaps 11;

Qy	11	LLSALLCRCQVDG--SGVFELKLQEFVNKKGLLSNRNCCRGGPGGAGQQQCDCKTFPRV	68	
Dd	5	MIAVLLCVMISQGFCSGVFELKLQEFLNKKGVGNANCKGSAAG--HQCECKTFPRI	61	
Qy	69	CLKHYQASVSPEPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWGTFS	128	
Dd	62	CLKHYQANVSPDPCTYGGAVTPVLGNSNFQVPSF--PDSSTNPPIPAFGFTWGTFS	119	
Qy	129	LIIEALHTDSPDDLTTENPERLISRATQRHLAVGEWSQDLHSSGRDCLKYSYRFVCD	188	
Dd	120	LIIEALHTDSTDDLSTENPDRLLISRMTTQRHLTVGEWSQDLQVGRTELKYSYRFVCD	179	
Qy	189	HYGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQGYCTEPICLPGCDEQHGFCDKPG	248	
Dd	180	HYGEGCSVFCRPRDDTFHFTCGERGEIICNSGWKQGYCTEPICLPGCDEHGFCDKPG	239	
Qy	249	ECKRVGWQGRYCDDECIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCKN	308	
Dd	240	ECKRVGFSKYCDDCIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCQNG	299	











Db 101 FSLIIESWTTNSAEQ-STENPDNLLSRLATRRRLSIGEDWSQDIHLGQQSELRYSYHVSC 159

Qy 187 DEHYYGEGCSVFCRPRDDRFHGHTCGERGEKVCNPGWKQYCTEPICLPGCDEQHGFCDK 246

Db 160 DEHYYGDSUSDYCRPRDDNFGHYTCDEQGNRLCMSGWKGEYCAEPICLPGCSESHGFCEL 219

Qy 247 PGECKRVGWQGRYCDERICYPGCLHGTCQQPWQCNQCEGWGGLFCNQDLNYCTHHKPCK 306

Db 220 PGECKRMGWQGELCDECLRYPGQHGSCSQPWECICQEGWGGLFCNQDLNYCTNHQPCR 279

Qy 307 NGATCTNTGQSYTCSRPGYTGSSCEIEINECDANPCKNKGGSCDLENSYSCTCPPGFY 366

Db 280 NGASCINTGQSYSCSRAGFTGTNCEIDINECASNPCKNKGGSCNDLENDYECVCRGFY 339

Qy 367 GKNCELSAMTCADGPCFNGGRCCTDNPDG-GYSCRCPLGYSGFNCEKKIDYCSSSSPCANGA 425

Db 340 GKNCDISAMTCEDGPCFNGGTCIEKSSGVGYVCRCPFNTHGSNCEKKIDRCTNSPCLNGG 399

Qy 426 QCVDLGNSYICQCQAGFTGRHCDNDNVDDCASFPVCVNGTQDGVNDYSCTCPPGYNGKNC 485

Db 400 QCLDMGRNVLCRCRPGFSGPRCELNIDDCASSPCANGGTCVDAVNSYTCSTLGYGGKDC 459

Qy 486 STPVSRCEHNPCHNGATCHERSNRYVCECARGYGGNLCQFLLPEPPQGPVIVDFTEKYTE 545

Db 460 TLRVDACSSKPKCKNGGTCYTHFTGNVCQCPTGFMGTSCEPRVHDPTPASHRADSSNTLT- 518

Qy 546 QONSQPPWIAVCAGIILVLMLLGCAAIWCVRLKVQKRHHQPEACRSETETMNNLANCQ 605

Db 519 -----MVCCLG--LLTFFLLGCGVMV--MRGMRRGH----- 546

Qy 606 REKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSVKEEHG 665

Db 547 -----FNEKGRVNDLEPKNLLIEKEPH-----FKMPNPDYLRKSS 583

Qy 666 KCEAKCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVVIVISEEKDECILIA 725

Db 584 SKQKLLQGSSE-EERSGRRTRDRKPDTKQCNPTSRY--PEDGAYHPIYIL-PEPEQCIFA 639

Qy 726 TEV 728

Db 640 TEV 642

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:11:34 ; Search time 75.9253 Seconds  
(without alignments)  
3411.281 Million cell updates/sec

Title: US-09-783-931-12  
Perfect score: 4121  
Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4007	97.2	722	2	AAW11720
2	4003	97.1	722	6	ABU55873
3	4003	97.1	722	6	AAE34029
4	3955	96.0	722	3	AAW79028
5	3659.5	88.8	723	2	AAW18353
6	3659.5	88.8	723	2	AAW75492
7	3659.5	88.8	723	2	AAW94498
8	3659.5	88.8	723	3	AAW83227
9	3659.5	88.8	723	3	AAW33422
10	3659.5	88.8	723	3	AAW24388
11	3659.5	88.8	723	3	AAW00172
12	3659.5	88.8	723	4	AAU12344
13	3659.5	88.8	723	4	AAW53064
14	3659.5	88.8	723	6	ABO17788
15	3659.5	88.8	723	6	ABU81042
16	3659.5	88.8	723	6	ABU66742
17	3659.5	88.8	723	6	ABU59823
18	3659.5	88.8	723	6	ABO25013
19	3659.5	88.8	723	6	ABU67018
20	3659.5	88.8	723	6	ADA45865
21	3659.5	88.8	723	6	ADA76296
22	3659.5	88.8	723	6	ADA18946
23	3659.5	88.8	723	6	ADA61569
24	3659.5	88.8	723	6	ADB19354
25	3659.5	88.8	723	6	ADB27895

26	3659.5	88.8	723	6	ADA86374	Ada86374	Novel hum
27	3659.5	88.8	723	6	ADB15938	ADB15938	Human PRO
28	3659.5	88.8	723	6	ADA47724	Ada47724	Human PRO
29	3659.5	88.8	723	6	ADA67519	Ada67519	Human PRO
30	3659.5	88.8	723	6	ADB30526	ADB30526	Human PRO
31	3659.5	88.8	723	6	ADA85822	Ada85822	Novel hum
32	3659.5	88.8	723	6	ADA97034	Ada97034	Human PRO
33	3659.5	88.8	723	6	ADA79338	Ada79338	Human PRO
34	3659.5	88.8	723	6	ADA87477	Ada87477	Novel hum
35	3659.5	88.8	723	6	ADB16679	ADB16679	Human PRO
36	3659.5	88.8	723	6	ADA91771	Ada91771	Novel hum
37	3659.5	88.8	723	6	ADB14834	ADB14834	Human PRO
38	3659.5	88.8	723	6	ADB18795	ADB18795	Novel hum
39	3659.5	88.8	723	6	ADA94010	Ada94010	Human PRO
40	3659.5	88.8	723	6	ADB19906	ADB19906	Novel hum
41	3659.5	88.8	723	6	ADB13218	ADB13218	Human PRO
42	3659.5	88.8	723	6	ABO43321	ABO43321	Novel hum
43	3659.5	88.8	723	6	ADA74472	Ada74472	Human PRO
44	3659.5	88.8	723	6	ADB24705	ADB24705	Human PRO
45	3659.5	88.8	723	6	ADA82229	Ada82229	Human PRO

ALIGNMENTS

RESULT 1  
AAW11720  
ID AAW11720 standard; protein; 722 AA.  
XX

AC AAW11720;

DT 28-APR-1997 (first entry)

XX M-Delta-1 polypeptide.

DE M-Delta-1; cell proliferation; nervous system disorder;  
KW tissue regeneration; Notch; cervix cancer; breast cancer;  
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

OS Mus sp.

XX WO9701571-A1.

PD 16-JAN-1997.

PF 28-JUN-1996; 96WO-US011178.

PR 28-JUN-1995; 95US-0000589P.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
(UYVA ) UNIV YALE.

PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;  
Gray GE;

XX WPI; 1997-100159/09.  
N-PSDB; AAT58899.

PT New vertebrate Delta protein, DNA and antibodies - for treating and  
preventing cancer, nervous system disorders and for tissue regeneration.

XX Claim 4; Fig 8; 135pp; English.

CC M-delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila  
Delta, a protein that binds to Notch protein. It is expressed primarily  
in presomitic mesoderm, the central and peripheral nervous systems, and  
kidney. Chick (AAW11719) and human (AAW11721- 38) Delta-1 polypeptides  
have also been identified. Delta-1 proteins can be used to treat or  
prevent disorders characterised by increased Notch activity, such as  
cervical, breast, lung or colon cancer, melanoma or seminoma, as well as  
nervous system disorders, and to promote tissue regeneration and repair

XX Sequence 722 AA;

Query Match		97.2%;	Score 4007;	DB 2;	Length 722;
Best Local Similarity		97.4%;	Pred. No. 2.2e-225;		
Matches 703;		Conservative 3;	Mismatches 16;	Indels 0;	Gaps 0;
QY	1	MGRRSALALAVVSALLCQVSSGVFELKLQEFVNKKGLGNRNCCRGSGPPCACRTFFR	60		
Db	1	MGRRSALALAVVSALLCQVSSGVFELKLQEFVNKKGLGNRNCCRGSGPPCACRTFFR	60		
QY	61	VCLKHYQASVSEPPCTYGSVAVPLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS	120		
Db	61	VCLKHYQASVSEPPCTYGSVAVPLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS	120		
QY	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE	180		
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE	180		
QY	181	HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGYCTDPICLPGCDDQHGYCDKPG	240		
Db	181	HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGYCTDPICLPGCDDQHGYCDKPG	240		
QY	241	ECKRVGWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG	300		
Db	241	ECKRVGWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG	300		
QY	301	ATCNTGQGSYTCSCRPGYTGANCELEVDCAKPCPKNGASCTDLEDSEFSCCTCPPGFYK	360		
Db	301	ATCNTGQGSYTCSCRPGYTGANCELEVDCAKPCPKNGASCTDLEDSEFSCCTCPPGFYK	360		
QY	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV	420		
Db	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV	420		
QY	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCRDSVNDSEFSCCTCPPGYTGKNCAP	480		
Db	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGTCRDSVNDSEFSCCTCPPGYTGKNCAP	480		
QY	481	VSRCEHAPCHNGATCHQRGORYMCECAQYGGPNCFLLPEPPPGPMVVDLSERHMESQG	540		
Db	481	VSRCEHAPCHNGATCHQRGORYMCECAQYGGPNCFLLPEPPPGPMVVDLSERHMESQG	540		
QY	541	GPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK	600		
Db	541	GPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK	600		
QY	601	DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK	660		
Db	601	DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK	660		
QY	661	RDTKCQSSQLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT	720		
Db	661	RDTKCQSSSAGEEKIAPTLRGGEIPDRKRPEVYSTSKDTKYQSVYVLSAEKDECVIAT	720		
QY	721	EV 722			
Db	721	EV 722			
RESULT 2					
ABU55873					
ID	ABU55873	standard; protein; 722 AA.			
XX	AC	ABU55873;			
XX	DT	25-MAR-2003 (first entry)			
XX	DE	Mouse notch ligand delta-like 1 protein.			

OS	Mus sp.
XX	WO200277204-A2.
PN	
XX	03-OCT-2002.
PD	
XX	25-MAR-2002; 2002WO-GB001195.
PF	
XX	23-MAR-2001; 2001GB-00007296.
PR	23-MAR-2001; 2001GB-00007299.
PR	17-APR-2001; 2001GB-00009346.
XX	(AXOR-) AXORDIA LTD.
PA	
XX	Andrews P, Walsh J, Gokhale P;
PI	
XX	WPI; 2003-092852/08.
DR	N-PSDB; ABX75296.
XX	
PT	Modulating the differentiation of embryonic stem cells by providing
PT	ligands which bind receptors in the Notch and Wnt pathways, useful for
PT	treating diseases such as Parkinson's, Huntington's, heart disease,
PT	diabetes and AIDS.
XX	
PS	Claim 6; Fig 3; 121pp; English.
XX	
CC	The invention relates to modulating the differentiation of an embryonic
CC	stem cell, comprising: (a) providing a culture of embryonic stem cells;
CC	(b) providing at least one ligand or its active binding fragment, capable
CC	of binding its cognate receptor polypeptide expressed by the embryonic
CC	stem cell; (c) forming a culture comprising embryonic stem cells and the
CC	ligand; and (d) growing the cell culture. Also included are: (1)
CC	Modulating the differentiation of embryonic stem cells, comprising: (a)
CC	providing a cell transfected with a nucleic acid molecule selected from:
CC	(i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic
CC	acid molecule that hybridises to the nucleic acid in (i), and which
CC	encodes a ligand capable of modulating embryonic stem cell
CC	differentiation, or capable of binding a Wnt receptor; or (iii) nucleic
CC	acid molecules which are degenerate as a result of the genetic code to
CC	the sequences of (i) or (ii); (b) forming a culture comprising the cell
CC	identified in (a) with an embryonic stem cell; and (c) growing the
CC	culture for the maintenance and/or differentiation of the embryonic stem
CC	cell; (2) Inhibiting the differentiation of embryonic stem cells,
CC	comprising: (a) providing at least one polypeptide or its active
CC	fragment, that are inhibitors of the Wnt signalling pathway; (b) forming
CC	a culture comprising the cell identified in (a) with an embryonic stem
CC	cell; and (c) growing the culture for the maintenance of embryonic stem
CC	cells in an undifferentiated state; or (3) Inhibiting the differentiation
CC	of embryonic stem cells, comprising: (a) providing a cell transfected
CC	with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt
CC	inhibitory polypeptide; (ii) a molecule which hybridises to the molecule
CC	of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;
CC	and (iii) nucleic acid molecules which are degenerate as a result of the
CC	genetic code to the sequences of (i) or (ii); (b) forming a culture
CC	comprising the cell identified in (a) with an embryonic stem cell; and
CC	(c) growing the culture for the maintenance of embryonic stem cells in an
CC	undifferentiated state; and (4) A cell, therapeutic cell or cell culture
CC	obtainable by any of the methods cited above. The therapeutic cell of the
CC	present invention is useful in the treatment of an animal, preferably a
CC	human, comprising administering a cell composition comprising embryonic
CC	stem cells which have been induced to differentiate into at least one
CC	cell-type. The cell is also useful for the manufacture of a composition
CC	for use in treatment of diseases such as Parkinson's disease,
CC	Huntington's disease, motor neuron disease, heart disease, diabetes,
CC	liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
CC	immunodeficiency syndrome). The present sequence is represents a Wnt or
CC	Notch pathway protein (i.e. a ligand for the method of the invention)
XX	
SQ	Sequence 722 AA;

Query Match 97.1%; Score 4003; DB 6; Length 722;  
Best Local Similarity 97.2%; Pred. No. 3.7e-225;  
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;



QY 1 MGRRSALALAVVSALLCQWSSGVFELKQLQEFVNVKKGLLGNRNCCRGSGGPPCACRTFFR 60  
DB 1 MGRRSALALAVVSALLCQWSSGVFELKQLQEFVNVKKGLLGNRNCCRGSGGPPCACRTFFR 60  
QY 61 VCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120  
DB 61 VCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120  
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVUDE 180  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVUDE 180  
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKPCRG 240  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKPCRG 240  
QY 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 300  
DB 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 300  
QY 301 ATCTNTGQSGYTCSRCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCCTPPGFY 360  
DB 301 ATCTNTGQSGYTCSRCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCCTPPGFY 360  
QY 361 VCELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSSPCSN 420  
DB 361 VCELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSSPCSN 420  
QY 421 DLGNSYLCRCQAGSFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480  
DB 421 DLGNSYLCRCQAGSFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480  
QY 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPPGPMVVDLSERH 540  
DB 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPPGPMVVDLSERH 540  
QY 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANCQ 600  
DB 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANCQ 600  
QY 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRD 660  
DB 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRD 660  
QY 661 RDTKCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDE 720  
DB 661 RDTKCQSQSAGEEKIAPTLRGGEIPDRKRPEVYSTSKDTKYQSVYVLSAEKDE 720  
QY 721 EV 722  
DB 721 EV 722  
RESULT 3  
ID AAE34029  
XX AAE34029 standard; protein; 722 AA.  
AC AAE34029;  
XX AAE34029;  
DT 02-MAY-2003 (first entry)  
XX Murine notch ligand delta-like 1 protein.  
DE Murine; drug screening; toxicology assay; signalling pathway;  
XX Murine notch ligand delta-like 1.  
KW Mus sp.  
XX WO200290992-A2.  
PN 14-NOV-2002.  
XX

PF 29-APR-2002; 2002WO-GB001946.  
XX 04-MAY-2001; 2001GB-00011004.  
PR (AXOR-) AXORDIA LTD.  
XX Andrews P, Draper J, Walsh J;  
PI WPI; 2003-120579/11.  
XX N-PSDB; AAD52523.  
DR Identifying biologically active agents comprises cloning transfected  
DR cells into a cell array, exposing the array to an agent to be tested, and  
XX detecting signals generated by a reporter molecule as a result of  
XX exposure to the agent.  
PS Claim 16; Fig 2; 90pp; English.  
XX The present invention relates to a novel screening method which enables  
CC the identification of biologically active agents which mediate their  
CC effect through the activation of genes. The method involves providing a  
CC population of cells stably transfected with a nucleic acid encoding a  
CC reporter molecule, cloning the transfected cells into a cell array,  
CC exposing the array to at least one agent to be tested and detecting a  
CC signal generated by the reporter molecule as a result of exposure to the  
CC agent. The method is useful in identifying biologically active agents and  
CC the genes through which the agents act, in screening potential drugs for  
CC their ability to activate certain drug targets in a high-throughput  
CC assay, in identifying relationships between signalling pathways and  
CC specific signals that could be useful in eventually directing the  
CC differentiation of embryonic stem cells and in toxicology assays by  
CC testing for unwanted activation or inhibition of specific signalling  
CC pathways. The present sequence is murine notch ligand delta-like 1  
CC protein used to illustrate the method of the invention  
XX  
SQ Sequence 722 AA;

Query Match 97.1%; Score 4003; DB 6; Length 722;  
Best Local Similarity 97.2%; Pred. No. 3.7e-225;  
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;  
QY 1 MGRRSALALAVVSALLCQWSSGVFELKQLQEFVNVKKGLLGNRNCCRGSGGPPCACRTFFR 60  
DB 1 MGRRSALALAVVSALLCQWSSGVFELKQLQEFVNVKKGLLGNRNCCRGSGGPPCACRTFFR 60  
QY 61 VCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120  
DB 61 VCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTFS 120  
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVUDE 180  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVUDE 180  
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKPCRG 240  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGKPCRG 240  
QY 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 300  
DB 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 300  
QY 301 ATCTNTGQSGYTCSRCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCCTPPGFY 360  
DB 301 ATCTNTGQSGYTCSRCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCCTPPGFY 360  
QY 361 VCELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSSPCSN 420  
DB 361 VCELSAMTCADGCPFCNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSSPCSN 420  
QY 421 DLGNSYLCRCQAGSFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480  
DB 421 DLGNSYLCRCQAGSFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480

QY 481 VSRCEHAPCHNGATCHQRGORYMCECAQGYGPNQCQFLLPEPPPGPMVVDLSERHMESQG 540  
Db |||||  
QY 541 GPPFWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGGETETMNNLANCQREK 600  
Dd |||||  
QY 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Dd |||||  
QY 661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Dd || : :  
QY 721 EV 722  
Dd ||  
QY 721 EV 722

RESULT 4  
AA79028  
ID AAY79028 standard; protein; 722 AA.  
XX  
AC AAY79028;  
DT 06-JUN-2000 (first entry)  
XX  
DE Murine delta protein amino acid sequence.  
XX  
KW Delta; Kuz; Notch; differentiation; cervical; breast; lung; cancer;  
KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;  
KW tissue regeneration; liver cirrhosis; keloid formation; baldness;  
KW inner ear disorder; mouse.  
XX  
OS Mus sp.  
XX  
PN WO200002897-A2.  
XX  
PD 20-JAN-2000.  
XX  
PF 13-JUL-1999; 99WO-US015817.  
XX  
PR 13-JUL-1998; 98US-0092513P.  
PR 19-OCT-1998; 98US-0104834P.  
XX  
PA (UYYA ) UNIV YALE.  
XX  
PI Artavanis-Tsakonas S, Rand MD, Qi H;  
XX  
DR WPI; 2000-282852/24.  
XX  
PT New cleavage peptide, nucleic acids and antibodies useful for diagnosis,  
PT prevention and treatment of cancer, disorders of central nervous system,  
PT cirrhosis and psoriasis.  
XX  
PS Claim 1; Fig 3; 177pp; English.

XX  
CC This sequence represents the murine delta protein amino acid sequence.  
CC Delta is a toporythmic protein that contains a sequence which is cleaved  
CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz  
CC results in two fragments, a soluble amino terminal fragment consisting  
CC essentially of the extracellular domain, and a membrane bound fragment  
CC consisting of the transmembrane domain and the intracellular domain. The  
CC soluble fragment is able to bind to Notch. Delta plays a key role in  
CC differentiation, and therefore detection and measurement of delta  
CC activation is important in the study of differentiation. The invention  
CC relates to the delta cleavage peptides (the active fragment), and to  
CC methods for detecting and measuring delta activation. Delta cleavage  
CC peptides, and chimeric proteins are useful for modulating the activity of  
CC Notch, delta or kuz or at least one of the signalling pathways in a cell  
CC or organism, expressing Notch. By contacting a cell with kuz protein or

CC nucleic acid or its antibody, the activity or levels of delta protein is  
CC modulated and vice versa. A delta cleavage peptide or its derivative  
CC capable of binding kuz protein is useful for treating or preventing a  
CC disease or disorder associated with increased delta activity or  
CC expression such as cervical, breast, colon or lung cancer, melanoma or  
CC seminoma in humans. A recombinant cell comprising a delta peptide is  
CC useful for treating or preventing central nervous system disorders. A  
CC delta cleavage peptide is useful for the diagnosis of diseases or  
CC disorders associated with increased levels of Notch-delta protein binding  
CC activity comprising measuring the ability of delta cleavage peptides in a  
CC sample to bind kuz protein. A complex of delta protein and kuz is useful  
CC for diagnosing or screening for the presence of, or predisposition to  
CC developing a disease or disorder associated with aberrant levels of the  
CC complex, comprising measuring the level or functional activity of the  
CC complex or RNA encoding delta or kuz in a sample. The delta cleavage  
CC peptide is also useful for promoting tissue regeneration and repair, for  
CC treating liver cirrhosis, keloid formation, psoriasis, baldness and  
CC degenerative or traumatic disorders of the sensory epithelium of the  
CC inner ear  
XX  
SQ Sequence 722 AA;

Query Match 96.0%; Score 3955; DB 3; Length 722;  
Best Local Similarity 96.1%; Pred. No. 2.3e-222;  
Matches 694; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MGRRSALALAVSALLCQVWSSGVFELKLOEFVNKKLLGNRNCCRGSGPPCACRTFFR 60  
Db |||||  
QY 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFNPPIRPFPGFTWPGTFS 120  
Dd |||||  
QY 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFNPPIRPFPGFTWPGTFS 120  
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLTLTGVGEWSQDLHSSGRTLRLYSYRFVUDE 180  
Dd LIIEALHTDSPDDLATENPERLISRLTTQRLTLTGVGEWSQDLHSSGRTLRLYSYRFVUDE 180  
QY 181 HYYGEGCSVFCRPDDAFGHFTCGDRGEKMDPGWKGOYCTDPICLPGCDDQHGKPCRG 240  
Dd ||||| : |||||  
QY 241 ECKCRVWGQGRYCDECIRYPGCVHGTCCQWPQCNCQBGWGLFCNQDLNYCTHHKPCRNG 300  
Dd ||||| : |||||  
QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCTCPPGFYK 360  
Dd ||||| : |||||  
QY 361 VCELSAMTCADGPCFNGGRCSNDPDGGYTCPLGFSGFNCEKMDLCGSSPSCNGAKCV 420  
Dd ||||| : |||||  
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
Dd ||||| : |||||  
QY 481 VSRCEHAPCHNGATCHQRGORYMCECAQGYGPNQCQFLLPEPPPGPMVVDLSERHMESQG 540  
QY 541 GPPFWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGGETETMNNLANCQREK 600  
Dd ||||| : |||||  
QY 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Dd ||||| : |||||  
QY 661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Dd ||||| : |||||

QY 721 EV 722  
Db 721 EV 722

RESULT 5  
AAW18353

ID AAW18353 standard; protein; 723 AA.  
XX  
AC AAW18353;  
XX  
DT 11-FEB-1998 (first entry)  
XX  
DE Proliferation and differentiation suppression polypeptide.  
XX  
KW Proliferation; differentiation; suppression; human; delta-1; serrate-1;  
blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /label= Signal  
FT Protein 22..723  
FT /label= Differentiation\_suppression\_protein  
XX  
PN W09719172-A1.  
XX  
PD 29-MAY-1997.  
XX  
PF 15-NOV-1996; 96WO-JP003356.  
XX  
PR 17-NOV-1995; 95JP-00299611.  
PR 30-NOV-1995; 95JP-00311811.  
XX  
PA (ASAH ) ASahi KASEI KOGYO KK.  
XX  
PI Sakano S, Itoh A;  
XX  
DR WPI; 1997-298110/27.  
DR N-PSDB; AAT70174.  
XX  
PT Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress  
proliferation and differentiation of undifferentiated human blood cells.  
XX  
PS Claim 15; Page 77-82; 114pp; Japanese.  
XX  
CC The present sequence represents a polypeptide which suppresses  
proliferation and differentiation of undifferentiated cells such as  
neurons and blood cells. The polypeptide may be used for the prevention  
and control of disorders involving undifferentiated cells, such as  
leukaemia and malignant tumours, and improvement of blood formation, e.g.  
after immunosuppression  
XX  
SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 2; Length 723;  
Best Local Similarity 87.0%; Pred. No. 3.8e-205;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRRSALAVSALLCQVSSGVFELKQEFVFNKKGLGNRNCCRGSG-PPCACRTFF 59  
Db 1 MGSRCALAVLSALLCQVSSGVFELKQEFVFNKKGLGNRNCCRGAGPPPCACRTFF 60

QY 60 RVCLKHYQASVSPPECTYGSATVPVLGVDSFSLPDGAGIDPAFNPFRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPPECTYGSATVPVLGVDSFSLPDGGGADSAFNPFRFPFGFTWPGTF 120

QY 120 SLIIIEALHTSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTDLRSYRFVCD 179  
Db 121 SLIIIEALHTSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKSYRFVCD 180

QY 180 EHYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGCDKP 239  
Db EHYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTEPICLPGCDDQHGCDKP 240

QY 240 GECKRVGWQGRYCDCEIRYPGVHGTCCQPWQCNQEGWGLFCNQDLNYCTHHKPCRN 299  
Db GECKRVGWQGRYCDCEIRYPGCLHGTCCQPWQCNQEGWGLFCNQDLNYCTHHKPCRN 300

QY 300 GATCTNTGQSYTCSRPGYTGANCELEVDCAKSPCKNGASCTDLEDSCPPGFGY 359  
Db GATCTNTGQSYTCSRPGYTGATCELGIDECDPSPCKNGGSCDLENSYCTCPPGFGY 360

QY 360 KVCELSAMTCADGPCFNGGRCSNDPGGYTCHPCPLGFGFNCCKMDLCSGSSPCSNKAKC 419  
Db KICELSAMTCADGPCFNGGRCSNDPGGYTCHPCPLGFGFNCCKMDLCSGSSPCSNKAKC 420

QY 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGYTGKNC 479  
Db VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDSVNDFSCTCPGYTGKNC 480

QY 480 PVSRCHEAPCHNGATCHQGRQYMCCECAQYGGPNCQFLLPEPPPGPMVVDLSERH 539  
Db PVSRCHEAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPEPPPGPAVVDLTK-LE 539

QY 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETMNNLANC 599  
Db GGPFPWAVCAGVILVLMLLGCAAVVVCVRLRLQKHRRPADPCRGETMNNLANC 599

QY 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGD 659  
Db KDVSYSIIIGATQIKNTNKKADFHGDHGAESKSFVKRYPTVDYNLVRDLKGD 659

QY 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFELTENRPESVYSTSKDTKYQSVVLSAEK 718  
Db KRDTKCQSQSGGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVVISEEK 719

QY 719 ATEV 722  
Db ATEV 723

RESULT 6  
AAW75492

ID AAW75492 standard; protein; 723 AA.  
XX  
AC AAW75492;  
XX  
DT 27-APR-1999 (first entry)  
XX  
DE Human delta-1 protein.  
XX  
KW Human; delta-1 protein; ligand; notch; drug; vascular cell; primer; PCR; amplification.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /note= "signal peptide"  
FT Protein 22..723  
FT /note= "mature delta-1 protein"

XX JP10316582-A.  
XX  
PD 02-DEC-1998.  
XX  
PF 14-MAY-1997; 97JP-00124062.  
XX  
PR 14-MAY-1997; 97JP-00124062.  
XX  
PA (ASAH ) ASahi KASEI KOGYO KK.  
XX  
DR WPI; 1999-076401/07.



DR N-PSDB; AAX16817.  
XX Vascular cell controlling agent comprises polypeptide - which is human  
PT notch ligand and is used as drug.  
XX  
XX  
PS Disclosure; Page 16-19; 21pp; Japanese.  
XX  
CC This sequence represents the human delta-1 protein, which is a ligand of  
CC the human notch protein. The protein or fragments, especially AAW75493-  
CC W75495, can be used as a drug to control vascular cells. The sequences  
CC were isolated and the truncated fragments were generated using the  
CC primers AAX16818-X16831  
XX  
SQ Sequence 723 AA;  
  
Query Match 88.8%; Score 3659.5; DB 2; Length 723;  
Best Local Similarity 87.0%; Pred. No. 3.8e-205;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
  
Qy 1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGAGPPPCACRTFF 60  
  
Qy 60 RVCLKHYQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGGGADSAFSPNIRFPFGFTWPGTF 120  
  
Qy 120 SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD 180  
  
Qy 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKGYCTDPICLPGCDDQHGYCDKP 239  
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240  
  
Qy 240 GECKRVGWQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCRN 299  
Db 241 GECKRVGWQGRYCDICIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300  
  
Qy 300 GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCCTCPPGPGY 359  
Db 301 GATCTNTGQGSYTCSCRPGYTGATCELIGIDEDPSPCKNGSGCTDLENSYSCTCPGPGY 360  
  
Qy 360 KVCBLSAMTCADGPCFNGGRCSNPDGGYTCCHPLGFSFNCEKMDLCGSSPSCNGAKC 419  
Db 361 KICBLSAMTCADGPCFNGGRCSNPDGGYSCRCPPVGYSGFNCEKKIDYCSSPSCNGAKC 420  
  
Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDSECTCPPGYTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDSVNDSECTCPPGYTGRNCSA 480  
  
Qy 480 PVSRCHEAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPMPMVVDLSERHMSQ 539  
Db 481 PVSRCHEAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLLEK-LEGQ 539  
  
Qy 540 GGPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQRE 599  
Db 540 GGPFPPWAVCAGVILVLLMLLGCAAVVCVRLRLQKRRPADPCRGETETMNNLANCQRE 599  
  
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAESKFVRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDVSYSIIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659  
  
Qy 660 KRDTKCSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 718  
Db 660 KRDTKCPQSGSSGEKGTPTTLRGEASERKRPDSGCSSTKDTKYQSVYVISEEKDECVI 719  
  
719 ATEV 722  
720 ATEV 723

RESULT 7

AAW94498  
ID AAW94498 standard; protein; 723 AA.  
XX  
AC AAW94498;  
XX  
DT 22-APR-1999 (first entry)  
XX  
DE Human delta-1 protein.  
XX  
KW Human; delta-1; delta-2; differentiation inhibitor; proliferation;  
KW leukaemia; malignant tumour.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /label= signal  
FT Protein 22..723  
FT /label= Delta-1  
XX  
PN WO9851799-A1.  
XX  
PD 19-NOV-1998.  
XX  
PF 13-MAY-1998; 98WO-JP002104.  
XX  
PR 14-MAY-1997; 97JP-00124064.  
XX  
PA (ASAH ) ASAH KASEI KOGYO KK.  
XX  
PI Sakano S;  
XX  
DR WPI; 1999-070120/06.  
DR N-PSDB; AAX16300.  
XX  
PT Peptide inhibiting the differentiation of undifferentiated blood - used  
PT for treatment of cancer and other disorders and the culture of human  
PT cells in vitro.  
XX  
PS Example 1; Page 64-69; 86pp; Japanese.  
CC  
CC The present invention describes full length and shortened human delta-2  
CC proteins. Human delta-2 is a differentiation inhibitor which inhibits the  
CC differentiation of undifferentiated cells (other than brain or muscle  
CC cells), such as blood cells, and enhances the proliferation of  
CC undifferentiated blood cells. Products of human delta-2 may be used for  
CC the treatment of diseases such as leukaemia and malignant tumours. They  
CC may also be used in the culture of human cells in vitro, e.g. for  
CC production of supplies of undifferentiated blood cells. The present  
CC sequence represents human delta-1, from an example of the present  
CC invention  
XX  
SQ Sequence 723 AA;  
  
Query Match 88.8%; Score 3659.5; DB 2; Length 723;  
Best Local Similarity 87.0%; Pred. No. 3.8e-205;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
  
Qy 1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGAGPPPCACRTFF 60  
  
Qy 60 RVCLKHYQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGGGADSAFSPNIRFPFGFTWPGTF 120  
  
Qy 120 SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD 180  
  
Qy 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKGYCTDPICLPGCDDQHGYCDKP 239  
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240



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QY 240 GECKCRVWGQRYCDECI RYPGCVHGTCCQPPWCNCQEGWGGLFCNQDLNYCTHHKPCRN 299
    |||||
Db 241 GECKCRVWGQRYCDECI RYPGCLHGTCCQPPWCNCQEGWGGLFCNQDLNYCTHHKPCKN 300
    |||||
QY 300 GATCTNTGQSYTCSRPGYT GANCELEVEDECAPSPCKNGASC TDLEDSFSCTCPPGFY 359
    |||||
Db 301 GATCTNTGQSYTCSRPGYT GATCELGIDECDPSCKNGGSC TDLENSVSCTCPPGFY 360
    |||||
QY 360 KVCELSAMTCADGPCFNGGRCS DNPDGGYTCHCPLGFSGFNCEKKMDLCSSSPCSNGAKC 419
    |||||
Db 361 KICELSAMTCADGPCFNGGRCS DSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC 420
    |||||
QY 420 VDLGNSYLRCQAGFSGRYCE DNVDDCASSPCANGGTCRDSV NDFSCTCPPGYTGNKCSA 479
    |||||
Db 421 VDLGDAYLRCQAGFSGRHCD DNVDDCASSPCANGGTCR DGVNDFSCTCPPGYTGRNCSA 480
    |||||
QY 480 PVSRCCEHAPCHNGATCH QRGORYMCECAQGYGPNQCQLLP EPPPGPMVVDLSERHMESQ 539
    |||||
Db 481 PVSRCCEHAPCHNGATCH ERHRYVCECARGYGPNCQFLLP ELPPGPAVVVDLTK-LEGQ 539
    |||||
QY 540 GGFPPWAVACAGVVLV LLLGCAAVVVCVRLKLOKHQPP PEPCCGETETMNNLANCQRE 599
    |||||
Db 540 GGFPPWAVACAGVILV LMLLLGCAAVVVCVRLQLQHRPP ADPCRGETETMNNLANCQRE 599
    |||||
QY 600 KDVSVSIIGATQIKNTN KKADFHDGHA EKSSFVKRYPTVDY NLVRLDKGDEATVRDTHS 659
    |||||
Db 600 KDISVSIIGATQIKNTN KKADFHDGHSADKNGFKARYPAVDY NLVQDLKGDDTAVRDAHS 659
    |||||
QY 660 KRDTKCQSQ-SLOEKRRSP QHLGVGRFLTENRPESVYSTS KOTKYQSVVYLSAEKDECVI 718
    |||||
Db 660 KRDTKCQPGSSGEBEKG TPTTLRGEASERKRPDSGCS TSOTKYQSVVYVISEEKDECVI 719
    |||||
QY 719 ATEV 722
    |||||
Db 720 ATEV 723

RESULT 8
AAY83227
ID AAY83227 standard; protein; 723 AA.
XX
AC AAY83227;
XX
DT 16-AUG-2000 (first entry)
XX
DE PRO172 Polypeptide.
KW Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
KW leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT Peptide 1. .21
FT /label= Signal_peptide
FT Modified-site 2. .8
FT /note= "N-myristoylation site"
FT Modified-site 37. .43
FT /note= "N-myristoylation site"
FT Modified-site 40. .46
FT /note= "N-myristoylation site"
FT Modified-site 93. .97
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 98. .104
FT /note= "N-myristoylation site"
FT Modified-site 99. .105
FT /note= "N-myristoylation site"
FT Modified-site 131. .135
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 154. .158
FT /note= "Casein kinase II phosphorylation"
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FT Modified-site 176. .185
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 203. .207
FT /note= "Casein kinase II phosphorylation site"
FT Domain 243. .255
FT /label= EGF-like_domain
FT Modified-site 252. .261
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 262. .268
FT /note= "N-myristoylation site"
FT Domain 274. .286
FT /note= "EGF-like domain"
FT Modified-site 281. .287
FT /note= "N-myristoylation site"
FT Modified-site 282. .288
FT /note= "N-myristoylation site"
FT Modified-site 301. .307
FT /note= "N-myristoylation site"
FT Modified-site 310. .316
FT /note= "N-myristoylation site"
FT Domain 314. .326
FT /label= EGF-like_domain
FT Modified-site 328. .334
FT /note= "N-myristoylation domain"
FT Modified-site 340. .346
FT /note= "N-myristoylation site"
FT Modified-site 342. .346
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 343. .355
FT /note= "Asn and Asp hydroxylation site"
FT Modified-site 344. .348
FT /note= "Casein kinase II phosphorylation site"
FT Domain 352. .364
FT /label= EGF-like_domain
FT Modified-site 369. .373
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 378. .384
FT /note= "N-myristoylation site"
FT Modified-site 387. .393
FT /note= "N-myristoylation site"
FT Domain 391. .403
FT /label= EGF-like_domain
FT Modified-site 420. .432
FT /note= "Asn and Asp hydroxylation site"
FT Domain 429. .441
FT /label= EGF-like_domain
FT Modified-site 457. .461
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 458. .480
FT /label= Asn and Asp hydroxylation site
FT Domain 467. .479
FT /label= EGF-like_domain
FT Modified-site 477. .481
FT /note= "N-glycosylation site"
FT Modified-site 483. .487
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 495. .499
FT /note= "Casein kinase II phosphorylation site"
FT Domain 505. .517
FT /label= EGF-like_domain
FT Modified-site 512. .518
FT /note= "N-myristoylation site"
FT Domain 548. .568
FT /label= Transmembrane_domain
FT Binding-site 552. .563
FT /label= Prokaryotic membrane lipoprotein lipid attachment
FT Modified-site 659. .663
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 660. .664
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Modified-site 670. .674
```





PR	08-MAR-1999;	99WO-US005028.	
PR	12-MAR-1999;	99US-0123957P.	
PR	28-APR-1999;	99US-0131445P.	
PR	14-MAY-1999;	99US-0134287P.	
PR	02-JUN-1999;	99WO-US012252.	
PR	23-JUN-1999;	99US-0141037P.	
PR	20-JUL-1999;	99US-0144758P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	01-SEP-1999;	99WO-US020111.	
PR	08-SEP-1999;	99WO-US020594.	
PR	13-SEP-1999;	99WO-US020944.	
PR	15-SEP-1999;	99WO-US021090.	
PR	15-SEP-1999;	99WO-US021547.	
PR	05-OCT-1999;	99WO-US023089.	
PR	29-OCT-1999;	99US-0162506P.	
XX			
PA	(GETH )	GENENTECH INC.	
XX			
PPI	Ashkenazi AJ,	Baker KP, Ferrara N,	Gerber H, Hillan KJ;
PPI	Goddard A,	Godowski PJ, Gurney AL,	Klein RD, Kuo SS, Paoni NF;
PPI	Smith V,	Watanabe CK, Williams PM,	Wood WI;
XX			
DR	WPI;	2000-412154/35.	
DR	N-PSDB;	AAA77512.	
XX			
PPT	Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing		
PPT	and treating diagnosing a cardiovascular, endothelial or angiogenic		
PPT	disorders in mammals.		
XX			
PS	Claim 72; Fig 2; 315pp; English.		
XX			
CCC	The present invention describes nucleic acids encoding PRO polypeptides		
CCC	useful for preventing, diagnosing and treating diagnosing a		
CCC	cardiovascular, endothelial or angiogenic disorder in mammals by		
CCC	modulating cell proliferation, angiogenesis and cardiovascularisation,		
CCC	and for identifying agonists and antagonists of these processes. The		
CCC	nucleic acids and the proteins they encode may be used in the prevention,		
CCC	treatment and diagnosis of diseases associated with inappropriate PRO		
CCC	expression such as cardiovascular, endothelial or angiogenic disorders in		
CCC	mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For		
CCC	example, the nucleic acids (NCs) and vectors containing them and the PRO		
CCC	polypeptide may be used to treat disorders associated with decreased PRO		
CCC	expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent		
CCC	nucleotide and protein sequences used in the exemplification of the		
CCC	present invention		
XX			
SQ	Sequence 723 AA;		
	Query Match	88.8%;	Score 3659.5; DB 3; Length 723;
	Best Local Similarity	87.0%;	Pred. No. 3.8e-205;
	Matches 630;	Conservative 46;	Mismatches 45; Indels 3; Gaps 3;
QY	1	MGRSALALAVSALLCQVWSSGVFELKIQEFVNKKGLGNRNCRRGGSG-PPCACKRTFF	59
Db	1	MGSRCALALAVLSALLCQVWSSGVFELKIQEFVNKKGLGNRNCRRGGAGPPPCACKRTFF	60
QY	60	RVCLKHYQASVSPEPCTYGSATPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF	119
Db	61	RVCLKHYQASVSPEPCTYGSATPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF	120
QY	120	SLIIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRSYRFVCD	179
Db	121	SLIIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD	180
QY	180	EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKP	239
Db	181	EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP	240
QY	240	GECKRVGWQGRYCDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRN	299
Db	241	GECKRVGWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCKN	300
QY	300	GATCTNTGGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCCTPPGFGY	359

Db	301	GATCTNTGGSYTCSCRPGYTGATCELGIDECDFSPCKNGSGSCTDLENSYSCTCPPPGFYG	360
Qy	360	KVCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPSCNGAKC	419
Db	361	KICELSAMTCADGPCFNGRCSDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSPSCNGAKC	420
Qy	420	VDLGN SylCRCAQGSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA	479
Db	421	VDLGDAYLCRCQAGSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCCTCPPGYTGRNCSA	480
Qy	480	PVSRCEHAPCHNGATCHORGQRYMCECAQGYGPNCOFLLPEPPPGPMVVDLSERHMESQ	539
Db	481	PVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCOFLLPELPPGPAVVDLTEK-LEGQ	539
Qy	540	GGPPFPWAVACGVVLVLLLLGCAAVVVCVRLKLOKHOPPPPEPCGGTETETMNNLANCQRE	599
Db	540	GGPPFPWAVACGVILVMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQRE	599
Qy	600	KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS	659
Db	600	KDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS	659
Qy	660	KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI	718
Db	660	KRDTKCQPOGSSGEEKGTPTTLRGGEASERKRPDGSGTSTKDTKYQSVYVISEEKDECVI	719
Qy	719	ATEV 722	
Db	720	ATEV 723	
RESULT 11			
AAB00172			
ID	AAB00172 standard; protein; 723 AA.		
XX	AAB00172;		
XX	08-FEB-2001 (first entry)		
DE	PRO172 polypeptide.		
KW	PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour;		
KW	treatment; therapy; agonist; antibody; breast cancer; ovarian cancer;		
KW	renal cancer; colorectal cancer; uterine cancer; prostate cancer;		
KW	lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;		
XX	anglogenic disorder; immunologic disorder; human.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1. .21	
FT	Modified-site	/label= Signal peptide	
FT		2. .8	
FT		/note= "N-myristoylation site"	
FT	Modified-site	37. .43	
FT		/note= "N-myristoylation site"	
FT	Modified-site	40. .46	
FT		/note= "N-myristoylation site"	
FT	Modified-site	93. .97	
FT		/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	98. .104	
FT		/note= "N-myristoylation site"	
FT	Modified-site	99. .105	
FT		/note= "N-myristoylation site"	
FT	Modified-site	131. .135	
FT		/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	154. .158	
FT		/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	176. .185	
FT		/note= "Tyrosine kinase phosphorylation site"	
FT	Modified-site	203. .207	
FT		/note= "Casein kinase II phosphorylation site"	







Db 1 MGSRCALALAVLSALLCQVWSSGVFELKLOEFVNVKKGILLGNRNCCRGAGPPPCACRTFF 60

QY 60 RVCLKHYQASVSPPEPCTYGSATVPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTF 119

Db 61 RVCLKHYQASVSPPEPCTYGSATVPVLGVDSFSLPDGGADSAFSNPPIRFPFGFTWPGTF 120

QY 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRLHTLVGEWSQDLHSSGRTDLRSYRFVCD 179

Db 121 SLIIIEALHTDSPDDLATENPERLISRLATQRLHTLVGEWSQDLHSSGRTDLKYSYRFVCD 180

QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGYCTDPICLPGCDDQHGVC DKP 239

Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFC DKP 240

QY 240 GECKCRVGMQGRYCD ECI RYPCGVHGTCCQWPQCQEGWGGLFCNQDLNYCTHHKPCRN 299

Db 241 GECKCRVGMQGRYCD ECI RYPCGLHGTCCQWPQCQEGWGGLFCNQDLNYCTHHKPCKN 300

QY 300 GATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLED SFSC TCPPGFYG 359

Db 301 GATCTNTGQGSYTCSCRPGYTGATCELGIDECDSPCKNGGSC TDL ENSYSCTCPPGFYG 360

QY 360 KVCELSAMTCADGPCFNGGRCSNDP DGGYTCHCPLGFSGFNCEKMDLCGSSPCSN GAKC 419

Db 361 KICELSAMTCADGPCFNGGRCS DSDPGGYSC RCPVGYSGFNCEKKIDYCSSPCSN GAKC 420

QY 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVND FSC TCPPGYTGKNCSA 479

Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSC TCPPGYTGRNCSA 480

QY 480 PVSRC E HAPCHNGATCHQRGQRYMCECAQGYGGPNQCFLLPEPPPGPMVVDLSERHMESQ 539

Db 481 PVSRC E HAPCHNGATCHRGHRYVCECARGYGGPNQCFLLPELP PGPVAVDLTEK-LEGQ 539

QY 540 GGPFPWVAVCAGVVLVLLJLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQRE 599

Db 540 GGPFPWVAVCAGVILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQRE 599

QY 600 KDVSVSIIGATQIKNTNKKADFHDGHGA EKSFEKVRYPYTVDYNLVRDLKGDEATVRDTHS 659

Db 600 KDISVSIIGATQIKNTNKKADFHDGHSADKNGFKARYPAVDYNLVQDLKGD TAVRDAHS 659

QY 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENPESVYSTSKDTKYQSVYVLSAEKDECVI 718

Db 660 KRDTKCQPQSGSGEKG TPTTLRGEASERKRBDSGCSTSKDTKYQSVYVISEKDECVI 719

QY 719 ATEV 722

Db 720 ATEV 723

RESULT 13

AAB53064

ID AAB53064 standard; protein; 723 AA..

XX AC AAB53064;

XX DT 28-FEB-2001 (first entry)

XX DE Human angiogenesis-associated protein PRO172, SEQ ID NO:2.

XX KW Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.

XX OS Homo sapiens.

XX PN WO200053753-A2.

XX

PD 14-SEP-2000.

XX 05-JAN-2000; 2000WO-US000219.

XX 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

XX (GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA; Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI; WPI; 2001-090793/10.

DR N-PSDB; AAC97368.

XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer.

PT

XX Claim 69; Fig 2; 293pp; English.

PS The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention

XX SQ Sequence 723 AA;

Query Match 88.8%; Score 3659.5; DB 4; Length 723;

Best Local Similarity 87.0%; Pred. No. 3.8e-205;

Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;



Qy 1 MGRSALALAVSALLCQVSSGVFELKLQEFVNKKGLGNRNCRRGGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCQVSSGVFELKLQEFVNKKGLGNRNCRRGGAGPPPCACRTFF 60

Qy 60 RVCLKHYQASVSPEPPCTYGSATPVVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSATPVVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF 120

Qy 120 SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD 180

Qy 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKGYCTDPICLPGCDDQHGYCDKP 239  
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240

Qy 240 GECKCRVGWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299  
Db 241 GECKCRVGWQGRYCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCKN 300

Qy 300 GATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTCPPPGFYG 359  
Db 301 GATCTNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGCTDLENSYSCTCPPPGFYG 360

Qy 360 KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPSCSNAKC 419  
Db 361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCVPVGYSGFNCEKKIDYCSSSPSCSNAKC 420

Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCHDDNVDDCASSPCANGGTCRGGVNDFSCTCPPGYTGRNCSA 480

Qy 480 PVSRCHEHAPCHNGATCHQGRQYMCECAQYGGPNCQFLLEPPPPGPMVVDLSEHNMESQ 539  
Db 481 PVSRCHEHAPCHNGATCHERHRYVCECARGYGGPNCQFLLELPFGPAVVDLLEK-LEGQ 539

Qy 540 GGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPECGGETETMNNLANCQRE 599  
Db 540 GGPFPWVAVCAGVILVLLMLLLGCAAVVVCVRLRLQKRRPPADPCRGETETMNNLANCQRE 599

Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDVSYSIIIGATQIKNTNKKADFHGDSADKNGFKARYPAVDYNLVRDLKGDDTAVRDAHS 659

Qy 660 KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVI 718  
Db 660 KRDTKCQSQSGSGEEKGTPTTLRGGEASERKRDPDSGCSTSKDTKYQSVYVISEEKDECVI 719

Qy 719 ATEV 722  
Db 720 ATEV 723

RESULT 14  
ABO17788  
ID ABO17788 standard; protein; 723 AA.  
XX  
AC ABO17788;  
XX  
DT 26-AUG-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO172.  
XX  
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;  
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
KW TNF-alpha release; cell proliferation; cell differentiation;  
KW gene expression modulator; proteoglycan release; cytokine release;  
KW tumour; inflammatory disease; organ failure; atherosclerosis;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
KW bioreactor; tissue typing.

XX Homo sapiens.  
OS  
XX  
PN US2003032156-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 06-MAY-2002; 2002US-00140474.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
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PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
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PR 18-FEB-2000; 2000WO-US004342.  
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PR 24-FEB-2000; 2000WO-US005004.  
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PR 02-MAR-2000; 2000WO-US005841.  
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PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
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PR 11-AUG-2000; 2000WO-US022031.



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PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
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PR 20-DEC-2000; 2000WO-US034956.  
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PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
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PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
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PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX

(GETH ) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
PI

XX WPI; 2003-341980/32.  
DR N-PSDB; ACD24025.

XX New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, acquired immunodeficiency  
PT syndrome (AIDS), or cancer.

XX Claim 12; Fig 346; 660pp; English.

PS The invention describes an isolated nucleic acid (I) comprising, or which  
XX has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences  
CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This is the amino acid sequence of a novel human secreted and

CC transmembrane PRO polypeptide  
XX  
SQ Sequence 723 AA;  
  
Query Match 88.8%; Score 3659.5; DB 6; Length 723;  
Best Local Similarity 87.0%; Pred. No. 3.8e-205;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
  
QY 1 MGRRSALALAVVSALLCQVWSSGVFELKIQEFVNKKGLLGNRNCCRGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCQVWSSGVFELKIQEFVNKKGLLGNRNCCRGAGPPPCACRTFF 60  
  
QY 60 RVCLKHYQASVSPPECTYGSATVPVLGVDSFSLPDGAGIDPAFSNPFRPFPGFTWPGTF 119  
Db 61 RVCLKHYQASVSPPECTYGSATVPVLGVDSFSLPDGGGADSAFSNPFRPFPGFTWPGTF 120  
  
QY 120 SLIIEALHTDSPDDLATENPERLISRLTTQRLHSLTVGEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIEALHTDSPDDLATENPERLISRLATQRLHSLTVGEWSQDLHSSGRTDLKYSYRFVCD 180  
  
QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKNCVDPGWKQYCTDPICLPGCDDQHGFCCKP 239  
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCCKP 240  
  
QY 240 GECKRVGWQGRYCDICIRYPGVHGTCCQPWQCNQCEGWGLFCNQDLNYCTHHKPCRN 299  
Db 241 GECKRVGWQGRYCDICIRYPGCLHGTCCQPWQCNQCEGWGLFCNQDLNYCTHHKPCKN 300  
  
QY 300 GATCTNTGGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCCTCPPGFY 359  
Db 301 GATCTNTGGSYTCSCRPGYTGATCELGDDECDPSPCKNGGSCDLENSYSCTCPPGFY 360  
  
QY 360 KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPGLFSGFNCCKMDLGGSSPCSNCAK 419  
Db 361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCCKIDYCSSSPCSNCAK 420  
  
QY 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCCTCPPGYTGRN 480  
  
QY 480 PVSRCHEAPCHNGATCCHQGRYMCCEAQQYGGPNCQFLLPEPPPGPMVVDLSERHME 539  
Db 481 PVSRCHEAPCHNGATCCHRGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTK-LEG 539  
  
QY 540 GGPFPMVAVCAGVWLVLALLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQ 599  
Db 540 GGPFPMVAVCAGVILVMLLLGCAAVVVCVRLRLQKHRRPADPCRGETETMNNLANCQ 599  
  
QY 600 KDVSVSIIGATQIKNTNKKADFHGDHGAEEKSSFVRYPTVDYNLVRLKGDDEATVRDTH 659  
Db 600 KDISVSIIGATQIKNTNKKADFHGDHSAADKNGFKARYPAVDYNLVQLKGGDDTAVRDA 659  
  
QY 660 KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVI 718  
Db 660 KRDTKCQSQSGSGEEKGTPTTLRGGEASERKRPSDSCSTSKDTKYQSVVISEEKDECVI 719  
  
QY 719 ATEV 722  
Db 720 ATEV 723

RESULT 15

ABU81042  
ID ABU81042 standard; protein; 723 AA.

XX ABU81042;

AC ABU81042;

XX 23-JUN-2003 (first entry)

XX Human PRO polypeptide #173.

DE Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;

KW

KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
KW hearing loss; coagulation disorder; stroke; heart attack; cardiant;  
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;  
KW antirheumatic; auditory; cerebroprotective; angiogenic.

XX Homo sapiens.

PN US2003004311-A1.

XX  
PD 02-JAN-2003.

XX  
PF 19-DEC-2001; 2001US-00028072.

XX  
PR 18-JUN-1997; 97US-0049911P.

PR 26-AUG-1997; 97US-0056974P.

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PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063082P.

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PR 28-OCT-1997; 97US-0063561P.

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PR 24-NOV-1997; 97US-0066511P.

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PR 10-SEP-1998; 98WO-US018824.

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PR 14-SEP-1998; 98WO-US019094.

PR 16-SEP-1998; 98WO-US019177.

PR 17-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
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PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
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PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
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PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.

XX (GETH ) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-352836/33.

DR N-PSDB; ACA67166.

XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid  
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or  
PT heart attack.

XX Claim 12; Fig 346; 643pp; English.

PS The present invention relates to the isolation of novel human PRO  
XX polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a medicament  
CC useful in the treatment of diabetes, bone and/or cartilage disorders  
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,  
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders  
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells, tissues or  
CC serum, and for affinity purification of PRO from recombinant cell culture  
CC or natural sources. ABU80870-ABU81144 represent the human PRO  
CC polypeptides of the invention. Note: The sequence data for this patent  
CC was obtained in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsdIDentry.html

XX Sequence 723 AA;

SQ

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QY	180	EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKGYCTDPICLPGCDDQHGYCDKP	239			
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QY	300	GATCTNTGGSYTCSCRPGYTGANCELEVDCA PSPCKNGASCTDLEDSFSCTCPPGFYG	359			
Db	301	GATCTNTGGSYTCSCRPGYTGATCELGIDECDFSPCKNGGSCDTLENSYSCTCPPGFYG	360			
QY	360	KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC	419			
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QY	420	VDLGN SYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDRSVNDFSCTCPPGYTGKNCSA	479			
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QY	719	ATEV 722				
Db	720	ATEV 723				

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OM protein - protein search, using sw model

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(without alignments)  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4121	100.0	722	4	US-09-908-322-12
3	3971	96.4	720	3	US-08-872-855-4
4	3840.5	93.2	713	3	US-08-872-855-5
5	3659.5	88.8	723	3	US-09-068-740A-9
6	3659.5	88.8	723	4	US-09-423-753-27
7	3659.5	88.8	723	4	US-10-140-002-346
8	3631.5	88.1	723	4	US-09-641-612-6
9	3571.5	86.7	702	3	US-09-068-740A-4
10	3368	81.7	728	3	US-08-981-392-2
11	3368	81.7	728	4	US-09-908-322-2
12	3357.5	81.5	729	3	US-08-872-855-8
13	3167.5	76.9	721	3	US-08-981-392-5
14	3167.5	76.9	721	4	US-09-908-322-5
15	3161.5	76.7	721	3	US-08-872-855-7
16	2837	68.8	520	3	US-09-068-740A-3
17	2823.5	68.5	717	3	US-08-872-855-9
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19	2462	59.7	578	4	US-09-908-322-13
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22	1879.5	45.6	685	4	US-09-423-753-25
23	1879.5	45.6	685	4	US-09-641-612-7
24	1879.5	45.6	685	4	US-10-140-002-88
25	1870	45.4	659	4	US-09-423-753-3
26	1654.5	40.1	500	4	US-09-423-753-2
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28	1468.5	35.6	833	1	US-08-083-590A-2	Sequence 2, Appli
29	1468.5	35.6	833	1	US-08-465-500-6	Sequence 6, Appli
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33	1468.5	35.6	833	3	US-08-893-828-6	Sequence 6, Appli
34	1463.5	35.5	832	4	US-08-981-392-6	Sequence 6, Appli
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36	1441.5	35.0	830	3	US-08-872-855-11	Sequence 11, Appl
37	1332.5	32.3	1218	2	US-08-400-159-6	Sequence 6, Appli
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41	1330.5	32.3	1193	2	US-08-400-159-10	Sequence 10, Appl
42	1330.5	32.3	1193	3	US-08-611-729A-10	Sequence 10, Appl
43	1330.5	32.3	1193	4	US-09-195-524-10	Sequence 10, Appl
44	1328.5	32.2	1219	3	US-08-882-046-5	Sequence 5, Appli
45	1328.5	32.2	1219	4	US-09-566-047-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
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; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 722 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-981-392-12

Query Match 100.0%; Score 4121; DB 3; Length 722;  
Best Local Similarity 100.0%; Pred. No.1.7e-301;  
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60  
Dbb 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60  
  
Qy 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
Dbb 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
  
Qy 121 LIIEALHTDSPDDLATENPERLISRLLTQRLHLLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
Dbb 121 LIIEALHTDSPDDLATENPERLISRLLTQRLHLLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
  
Qy 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240  
Dbb 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240  
  
Qy 241 ECKCRVGMQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
Dbb 241 ECKCRVGMQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
  
Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTCPPGFYK 360  
Dbb 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTCPPGFYK 360  
  
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Dbb 361 VCELSAMTCADGPGCFNGGRCSNDPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420  
  
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
Dbb 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
  
Qy 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPBPFGPMVVDLSERHMSQG 540  
Dbb 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPBPFGPMVVDLSERHMSQG 540  
  
Qy 541 GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETMNNLANCQREK 600  
Dbb 541 GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETMNNLANCQREK 600

RESULT 2

US-09-908-322-12  
; Sequence 12, Application US/09908322  
; Patent No. 6783956  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/908,322  
FILING DATE: 17-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/981,392  
FILING DATE: 22-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 722 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-908-322-12

Query Match 100.0%; Score 4121; DB 4; Length 722;  
Best Local Similarity 100.0%; Pred. No. 1.7e-301;  
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60  
Dbb 1 MGRSALALAVVSALLCQVSSGVFELKLOEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60  
  
Qy 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
Dbb 61 VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
  
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Dbb 121 LIIEALHTDSPDDLATENPERLISRLLTQRLHLLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
  
Qy 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240  
Dbb 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240  
  
Qy 241 ECKCRVGMQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
Dbb 241 ECKCRVGMQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
  
Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTCPPGFYK 360  
Dbb 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTCPPGFYK 360  
  
Qy 361 VCELSAMTCADGPGCFNGGRCSNDPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420  
Dbb 361 VCELSAMTCADGPGCFNGGRCSNDPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420  
  
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
Dbb 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
  
Qy 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPBPFGPMVVDLSERHMSQG 540  
Dbb 481 VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCQFLLPBPFGPMVVDLSERHMSQG 540  
  
Qy 541 GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETMNNLANCQREK 600  
Dbb 541 GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPCGGTETMNNLANCQREK 600



; INFORMATION FOR SEQ ID NO: 5:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 713 amino acids									
; TYPE: amino acid									
; STRANDEDNESS:									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
US-08-872-855-5									
Query Match 93.2%; Score 3840.5; DB 3; Length 713;									
Best Local Similarity 93.4%; Pred. No. 2e-280;									
Matches 674; Conservative 11; Mismatches 28; Indels 9; Gaps 2;									
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Db	1	MGRSALALAVSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPC	ACRTFFR	60					
QY	61	VCLKHYQASVSPEPPCTYGS	AVTPVLGVDSFSLPDGAGIDPAFSNP	IRFPFGFTWPGTFS	120				
Db	61	VCLKHYQASVSPEPPCTYGS	AVTAVLGVDSFSLPDGAGIDPAFSNP	IRFPFGFTWPGTFS	120				
QY	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGE	WSQDLHSSGRTDLRYSYRFV	CDE	180				
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRH-TVGE	WSQDLHSSGRTDLRYSYRFV	CDE	179				
QY	181	HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMC	DPGWKGYCTDPICLPGCDDQHGYCDKPG	240					
Db	180	HYYGEGCSVFCRPRDDAFGHFTCGERGEKMC	DPGWKGYCTDPICLPGCDDQHGYCDKPG	239					
QY	241	ECKCRVWQGRYCD	CIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC	RNG	300				
Db	240	ECKCRVWQGRYCD	CIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC	RNG	299				
QY	301	ATCTNTGQGSYTC	SCRPGYTGANCELEVDECAPSPCKNGASCTDLED	SFSC	360				
Db	300	ATCTNTGQGSYTC	SCRPGYTGANCELEVDECAPSPCKNGGSC	CTDLED	359				
QY	361	VCELSAMTCADGPC	FCNFGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPC	SNAGKCV	420				
Db	360	VCELSAMTCADGPC	FCNFGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSP	PCSNAGKCV	419				
QY	421	DLGNSYLCRCQAG	FSGRYCEDNVDDCASSPCANGGTCRDSVND	FSCTCP	480				
Db	420	DLGNSYLCRCQ	TGFSGRYCEDNVDDCASSPCANGGTCRDSVND	FSCTCP	479				
QY	481	VSRCEHAPCHNGAT	CHQRGORYMCECAQGYGGPNCQFLLP	PEPPPGPMVVDL	540				
Db	480	VSRCEHAPCHNGAT	CHQRGORYMCECAQGYGGANCQFLLP	PEPPDLIVA	531				
QY	541	GPFPWAVACGV	LVLLLLLGGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANC	QREK	600				
Db	532	GSFPWAVACGV	LVLLLLLGGCAAVVVCVRLKLQKHQPPDP	CGGETETMNNLANC	591				
QY	601	DVSVSIIGATQIK	TNKKADFHGDHGA	EKSSFKVRYPTVDYNLVRDLKGDEATVRD	660				
Db	592	DVSVSIIGATQIK	TNKKADFHGDHGA	EKSSFKARYPTVDYNLIRDLKGDEATVR	651				
QY	661	RDTKCQSQLQEK	RRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEK	DECVIAT	720				
Db	652	RDTKCQSGSAGE	EKSTSLRGGEVDPDRKRPESVYSTSKDTKYQSVVLSAEK	DECVIAT	711				
QY	721	EV	722						
Db	712	EV	713						
RESULT 5									
US-09-068-740A-9									
; Sequence 9, Application US/09068740A									
; Patent No. 6337387									
; GENERAL INFORMATION:									
; APPLICANT: SAKANO, SEIJI									
; APPLICANT: ITOH, AKIRA									

; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE									
; FILE REFERENCE: KP-8447									
; CURRENT APPLICATION NUMBER: US/09/068,740A									
; CURRENT FILING DATE: 1998-06-18									
; PRIOR APPLICATION NUMBER: JP 7-299611									
; PRIOR FILING DATE: 1995-11-17									
; PRIOR APPLICATION NUMBER: JP 7-311811									
; PRIOR FILING DATE: 1995-11-30									
; PRIOR APPLICATION NUMBER: PCT/JP96/03356									
; PRIOR FILING DATE: 1996-11-15									
; NUMBER OF SEQ ID NOS: 48									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 9									
; LENGTH: 723									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-068-740A-9									
Query Match 88.8%; Score 3659.5; DB 3; Length 723;									
Best Local Similarity 87.0%; Pred. No. 8e-267;									
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;									
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Db	1	MGRSALALAVLSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGAGP	PPCACRTFF	60					
QY	60	RVCLKHYQASVSPEPPCTYGS	AVTPVLGVDSFSLPDGAGIDPAFSNP	IRFPFGFTWPGTF	119				
Db	61	RVCLKHYQASVSPEPPCTYGS	AVTPVLGVDSFSLPDGGGADSAFSNP	IRFPFGFTWPGTF	120				
QY	120	SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGE	WSQDLHSSGRTDLRYSYRFV	CD	179				
Db	121	SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGE	WSQDLHSSGRTDLKYSYRFV	CD	180				
QY	180	EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMC	DPGWKGYCTDPICLPGCDDQHGYCDK	P	239				
Db	181	EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVC	NPGWKGPYCTEPICLPGCDEQHGFCDK	P	240				
QY	240	GECKCRVWQGRYCD	CIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC	RN	299				
Db	241	GECKCRVWQGRYCD	CIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC	KN	300				
QY	300	GATCTNTGQGSYTC	SCRPGYTGANCELEVDECAPSPCKNGASCTDLED	SFSC	359				
Db	301	GATCTNTGQGSYTC	SCRPGYTGATCELGIDECDPSPCKNGGSC	CTDLENSYSCTCP	360				
QY	360	KVCELSAMTCADGPC	FCNFGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPC	SNAGK	419				
Db	361	KICELSAMTCADGPC	FCNFGRCSDSPDGGYSCRPCVGYSGFNCEKKIDYCSSSP	PCSNAGK	420				
QY	420	VDLGNSYLCRCQAG	FSGRYCEDNVDDCASSPCANGGTCRDSVND	FSCTCP	479				
Db	421	VDLGDAYLCRCQAG	FSGRHCDNVDDCASSPCANGGTCRDGVND	FSCTCP	480				
QY	480	PVSRCEHAPCHNGAT	CHQRGORYMCECAQGYGGPNCQFLLP	PEPPPGPMVVDL	539				
Db	481	PVSRCEHAPCHNGAT	CHERHRYVCECARGYGGPNCQFLLP	PELPPGPAVVDL	539				
QY	540	GGPFPWAVACGV	LVLLLLLGGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANC	QRE	599				
Db	540	GGPFPWAVACGV	LVLMLLLGGCAAVVVCVRLRLQKHPPADPCR	GETETMNNLANC	599				
QY	600	KDVSYSIIIGATQIK	TNKKADFHGDHGA	EKSSFKVRYPTVDYNLVRDLKGDEATVRD	659				
Db	600	KDISVSIIGATQIK	TNKKADFHGDHSA	DKNGFKARYPAVDYNLVDLKGDDTAVR	659				
QY	660	KRDTKCQSQ-SLQEK	RRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEK	DECVI	718				
Db	660	KRDTKCQPQGS	GEEKGTPTTLRGGEASERKR	RPDSGCTSKDTKYQSVYVISEEK	719				
QY	719	ATEV	722						
Db	720	ATEV	723						





Db 361 KICELSAMTCADGPCFNGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC 420  
Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGRNCSA 480  
Qy 480 PVSRCHEAPCHNGATCHORQORYMCECAQYGGPNCFLLPEPPPGPMVVDLSERHMESQ 539  
Db 481 PVSRCHEAPCHNGATCHERHRYVCECARGYGGPNCFLLPELPPGPAVVDLLEK-LEGQ 539  
Qy 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQRE 599  
Db 540 GGPFPWAVCAGVILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQRE 599  
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDISYSIIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659  
Qy 660 KRDTKCQSQ-SLQEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVI 718  
Db 660 KRDTKCQPQSGSGEEKGTPTTLRGEASERKRPDSCSTSKDTKYQSVYVISEEKDECVI 719  
Qy 719 ATEV 722  
Db 720 ATEV 723

RESULT 8  
US-09-641-612-6  
; Sequence 6, Application US/09641612  
; Patent No. 6703221  
; GENERAL INFORMATION:  
; APPLICANT: Vivien Chan et al.  
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF  
; FILE REFERENCE: PPO-1602.002 / 200130.498  
; CURRENT APPLICATION NUMBER: US/09/641,612  
; CURRENT FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-641-612-6

Query Match 88.1%; Score 3631.5; DB 4; Length 723;  
Best Local Similarity 86.5%; Pred. No. le-264;  
Matches 626; Conservative 46; Mismatches 49; Indels 3; Gaps 3;

Qy 1 MGRRSALALAVVSALLCOVWSSGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCOVWSSGVFELKLOEFVNKKGLGNPNCCRGAGPPPCACRTFF 60  
Qy 60 RVCLKHYQASVSPEPPCTYGSVATPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSVATPVLGVDSFSLPDGAGDASAFSNPIRFPFGFTWPGTF 120  
Qy 120 SLIIIEALHTDSPDDLATENPERLISRLLTQRHLTVGEWSQDLHSSSGRTDLRYSYRFVCD 179  
Db 121 SLIIIEALHTDSPDDLATENPERLISPLATQRHLTVGEWSQDLHSSSGRTDLKYSYRFVCD 180  
Qy 180 EHYVGECSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKP 239  
Db 181 EHYVGECSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240  
Qy 240 GECKCRVWQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299  
Db 241 GECKCRVWQGRYCDICIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCKN 300  
Qy 300 GATCTNTGQSYTCSRCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSEFSCTCPPGFY 359  
Db 301 GATCTNTGQSYTCSRCRPGYTGATCELGIDECDPSPCKNGSGSCTDLENSYCTCPPGFY 360

Qy 360 KVCELSAMTCADGPCFNGRCSDNPDDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC 419  
Db 361 KICELSAMTCADGPCFNGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC 420  
Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGRNCSA 480  
Qy 480 PVSRCHEAPCHNGATCHORQORYMCECAQYGGPNCFLLPEPPPGPMVVDLSERHMESQ 539  
Db 481 PVSRCHEAPCHNGATCHERHGHYVCECARGYGGPNCFLLPELPPGPAVVDLLEK-LEGQ 539  
Qy 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQRE 599  
Db 540 GGPFPWAVCAGVILVLMLLGCAAVVVCVPLRLQKHRPPADPCRGETETMNNLANCQRE 599  
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDISYSIIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659  
Qy 660 KRDTKCQSQ-SLQEKRRSPQHLGVRFLTENRPESVYSTSKDTKYQSVVYLSAEKDECVI 718  
Db 660 KRDTKCQPQSGSGEEKGTPTTLRGEASERKRPDSCSTSKDTKYQSVYVISEEKDECVI 719  
Qy 719 ATEV 722  
Db 720 ATEV 723

RESULT 9  
US-09-068-740A-4  
; Sequence 4, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 702  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-4

Query Match 86.7%; Score 3571.5; DB 3; Length 702;  
Best Local Similarity 87.1%; Pred. No. 3.2e-260;  
Matches 612; Conservative 45; Mismatches 43; Indels 3; Gaps 3;

Qy 22 SGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCACRTFFRVCLKHYQASVSPEPPCTYGS 80  
Db 1 SGVFELKLOEFVNKKGLGNRNCRRGGAGPPPCACRTFFRVCLKHYQASVSPEPPCTYGS 60  
Qy 81 AVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFSLIIIEALHTDSPDDLATENPE 140  
Db 61 AVTPVLGVDSFSLPDGAGDASAFSNPIRFPFGFTWPGTFSLIIIEALHTDSPDDLATENPE 120  
Qy 141 RLISRLLTQRHLTVGEWSQDLHSSSGRTDLRYSYRFVCDHYHGGCSVFCRPRDDAFGH 200  
Db 121 RLISRLLATQRHLTVGEWSQDLHSSSGRTDLKYSYRFVCDHYHGGCSVFCRPRDDAFGH 180  
Qy 201 FTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPGECKCRVWQGRYCDICIRYP 260  
Db 181 FTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGRYCDICIRYP 240









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Db 1 MGGRFLLTLALLSALLCRQVDGSGVFELKLQEFVFNKKGLLSNRNCCRGG-GPGAGQQQ 59
Qy 53 CACRTFFRVCLKHYSQASVSPPEPCTYGSVATPVLGVDVSFSLPDGA-GIDPAFSNPIRFPF 111
Db 60 CDCKTFFRVCLKHYSQASVSPPEPCTYGSAITPVLGANSFSVPDAGGADPAFSNPIRFPF 119
Qy 112 GFTWPGTFSLLIEALHTDSPDDLATENPERLISRLTQRHLLTVGEWSQDLHSSGRDCLR 171
Db 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRDCLK 179
Qy 172 YSYRFVCDHYHGGCVSFCRPRDDAFGHFTCGRGEKMDPGWKQYCTDPICLPGCDD 231
Db 180 YSYRFVCDHYHGGCVSFCRPRDDRFHFCTGGERGEKVCNPNWKQYCTEPICLPGCDE 239
Qy 232 QHGYCDKPGECKRVLGQGRYCDICIRYPGCVHGTCCQPPWCNQCQEGWGLFCNQDLNYC 291
Db 240 QHGFCDKPGECKRVLGQGRYCDICIRYPGCLHGTCCQPPWCNQCQEGWGLFCNQDLNYC 299
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Db 300 THHKPCNATCTNTGQGSYTCSCRPGYTGSSCSIEINECDANPCNKGSCSTDLENSYSC 359
Qy 352 TCPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSS 411
Db 360 TCPPGFYGKNCELSAMTCADGPCFNGGRCRDNPDGGYSCRCPLGYSGFNCEKIDYCSSS 419
Qy 412 PCSNGAK-CVDLGNLYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPP 470
Db 420 PCANGAACVDLGNLYLCQAGFTGRHCDNVDDCASFPVCVNGGTCQDGVNDYSCTCPP 479
Qy 471 GYTGKNCAPVSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPGPMVVD 530
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Qy 531 LSERHMESQGGPFPPVAVCAGVLVLLLLGCAAUVVVCVRLKLQKHQPPPEPCGGETETM 590
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RESULT 13
US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-5

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Qy 58 FERVCLKHYSQASVSPPEPCTYGSVATPVLGVDVSFSLPDGAGIDPAFSNPIRFPFTWPG 117
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Qy 298 RENGATCTNTGQGSYTCSCRPGYTGANCELEVDDECAPSPCKNGASCSTDLEDSFSCTPPGF 357
Db 301 ENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDANPCNKGSCSDLENSYTCSCPPGF 360
Qy 358 YGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCCHPLGFSGFNCEKMDLCGSSPCSNGA 417
Db 361 YGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCEKIDYCSSNPCANGA 420
Qy 418 KCVDLGNLYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 477
Db 421 RCEDLGNLYLCQCEGFSGRNCDNLDCTSFPCQNGGTCQDGINDYSCTCPGYIGKNC 480
Qy 478 SAPVSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPGPMVVDLSERHME 537
Db 481 SMPITKCEHNPCHNGATCHERNRNVYVQCARGYGGNCCQFLLPEEK--PVVVDLTKYTE 538
Qy 538 SQGGPFPPVAVCAGVLVLLLLGCAAUVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQ 597
Db 539 GQSGQFPWIAVCAGIVLMLLLGCAAUVVVCVVRVVRVQKRHHQPEACRGSKTMNNLANCQ 598
Qy 598 REKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDT 657
Db 599 REKDISVFIGTTQIKNTNKKIDFLSENNKNGYKPRYPSVDYNLVHELKVEDSP-KEE 657
Qy 658 HSKRDTKCQS-----QSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVL 709
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; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 721 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-855-7

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				Indels	23;
				Gaps	5;
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QY	58	FFRVCLKHYQASVSPPEPCTYGSAVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPG			117
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QY	178	CDEHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCCDDQHGYCD			237
Db	181	CDEYYYGEGCSYCRPRDDAFGHFSCGEGKGNLCNPGWKGLYCTEPICLPGCDEHHGYCD			240
QY	238	KPGECKCRVGNQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPC			297
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QY	298	RNGATCTNTGGSYTCSCRPGYTGANCELEVEDCAPSPCKNGASCCTDLEDSFSCTCPPGF			357
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QY	358	YGKVCELSAMTCADGPCFNGGRCSNDPDDGYTCHCPLGSGFNCEKMDLCGSSPCSNGA			417
Db	361	YGKNCELSAMTCADGPCFNGGRCADNPDDGYICPCPVGYSGFNCEKKIDYCSSNPCANGA			420
QY	418	KCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC			477
Db	421	RCEDLGNSYICQCQEGFSGRNCDNDLDDCTSFPCQNGGTCQDGINDYSCTCPPIYIGKNC			480
QY	478	SAPVSRCEHAPCHNGATCHQGRQRYMCEAQYGGPNCQFLLPEPPGPMVVDLSERHME			537
Db	481	SMPITKCEHNPCHNGATCHERNRNVYQCARGYGGNNCQFLLPEEK--PWVVDLTEKYTE			538
QY	538	SQGGPFPPWAVCAGVVLVLLLLGCAAUVVVCVRLKLOKHQPPPEPCGETETMNNLANCQ			597
Db	539	QSGQFPWIAVCAGIVLVMLLLGCAAUVVVCVVRVVRVQRRHQPEACRGESKTMNNLANCQ			598
QY	598	REKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDT			657
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QY	658	HSKRDTKCQS-----QSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVL			709
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QY	710	SAEKDECVIATEV			722
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 72.7322 Seconds  
(without alignments)  
3520.994 Million cell updates/sec

Title: US-09-783-931-12  
Perfect score: 4121  
Sequence: 1 MGRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4121	100.0	722	9	US-09-908-322-12 Sequence 12, Appl
2	4121	100.0	722	10	US-09-783-931-12 Sequence 12, Appl
3	4003	97.1	722	15	US-10-042-865-107 Sequence 107, App
4	4003	97.1	722	16	US-10-731-741-4 Sequence 4, Appli
5	3971	96.4	720	14	US-10-417-719-4 Sequence 108, App
6	3848	93.4	714	15	US-10-042-865-108 Sequence 5, Appli
7	3840.5	93.2	713	14	US-10-417-719-5 Sequence 21, Appl
8	3659.5	88.8	723	9	US-09-828-366-21 Sequence 9, Appli
9	3659.5	88.8	723	9	US-09-995-593A-9 Sequence 346, App
10	3659.5	88.8	723	14	US-10-028-072-346 Sequence 346, App
11	3659.5	88.8	723	14	US-10-140-808-346 Sequence 346, App
12	3659.5	88.8	723	14	US-10-121-049-346 Sequence 346, App
13	3659.5	88.8	723	14	US-10-123-904-346 Sequence 346, App

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39	3659.5	88.8	723	14	US-10-124-822-346 Sequence 346, App
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41	3659.5	88.8	723	14	US-10-160-498-346 Sequence 346, App
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43	3659.5	88.8	723	14	US-10-127-825A-346 Sequence 346, App
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45	3659.5	88.8	723	14	US-10-127-835A-346 Sequence 346, App

ALIGNMENTS

RESULT 1  
US-09-908-322-12  
; Sequence 12, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henriquez, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12

Query Match      100.0%; Score 4121; DB 9; Length 722;
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Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120

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Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180

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Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDDQHGYCDKPG 240

QY 241 ECKCRVWGQGRYCYDECIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
Db 241 ECKCRVWGQGRYCYDECIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300

QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSEFSCTCPPGFYGK 360
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QY 361 VCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCEKKMDLCGSSPCSNCAKCV 420
Db 361 VCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCEKKMDLCGSSPCSNCAKCV 420

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; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-783-931-12
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Query Match      100.0%; Score 4121; DB 10; Length 722;
Best Local Similarity 100.0%; Pred. No. 4.3e-272;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60
Db 1 MGRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSGPPCACRTFFR 60

QY 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120
Db 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120

QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180

QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDDQHGYCDKPG 240
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDDQHGYCDKPG 240

QY 241 ECKCRVWGQGRYCYDECIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
Db 241 ECKCRVWGQGRYCYDECIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300

QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSEFSCTCPPGFYGK 360
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Db	301	ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYK	360
QY	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPSCSNGAKCV	420
Db	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPSCSNGAKCV	420
QY	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC SAP	480
Db	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC SAP	480
QY	481	VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCOFLPEPPPGPMVVDLSERHMESQ	540
Db	481	VSRCEHAPCHNGATCHQGRQRYMCECAQYGGPNCOFLPEPPPGPMVVDLSERHMESQ	540
QY	541	GPFPWAVCAGVVLVLLLLGCAA VVVCVRLKLQKHQPPPEPCGGTETMNNLANCQREK	600
Db	541	GPFPWAVCAGVVLVLLLLGCAA VVVCVRLKLQKHQPPPEPCGGTETMNNLANCQREK	600
QY	601	DVSVSIIGATQIKNTNKKADPHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK	660
Db	601	DVSVSIIGATQIKNTNKKADPHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK	660
QY	661	RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT	720
Db	661	RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT	720
QY	721	EV 722	
Db	721	EV 722	

### RESULT 3

US-10-042-865-107  
; Sequence 107, Application US/10042865  
; Publication No. US20040029216A1

GENERAL INFORMATION:

**APPLICANT: Padigaru. Muralidhara**

APPLICANT: Li, Li

APPLICANT: Zerhusen, Bryan D

APPLICANT: CASMAN

**APPLICANT:** Shenoy.

; AFFILIANT: smenoy, suresh  
: APPLICANT: kimberly  
: APPLICANT: spvtek

APPLICANT: Zhong Mei

; APPLICANT: ZHONG, MEI  
: APPLICANT: Gaoqin; Esba A

APPLICANT: GARGOLI, Esha A

APPLICANT: BURGESS, Catherine

APPLICANT: Varnot Corina

APPLICANT: Vernet, Corinne

APPLICANT: Taylor, Sarah

APPLICANT: Tchernev, Velizar

; APPLICANT: Miller, Charles

APPLICANT: Guo, Xiaojia

; APPLICANT: Boldog, Ferenc L

APPLICANT: Grosse, William M

APPLICANT: Alsobrook II, John

; APPLICANT: Gerlach, Valerie L

APPLICANT: Edinger, Shlomit

APPLICANT: Rothenberg, Ma

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John

APPLICANT: Malyankar, Uriel

APPLICANT: Millet. Isabel

APPLICANT: **peyman, John**

APPLICANT: **SMITHSON. GLENN**

APPLICANT: Gunther, Erik

APPLICANT: Stone David  
AFFILIANT: Guilmer, Erik

APPLICANT: STONE, DAVID  
TITLE OF INVENTION: Proteins Polym

TITLE OF INVENTION:	PLOCE
TITLE OF INVENTION:	USIN
TITLE OF INVENTION:	

1. TITLE OF INVENTION: USING THE SAME  
2. FILE REFERENCE: 21402-527

FILE REFERENCE: 21402-537

;; CURRENT APPLICATION NUMBER: US/10/04

; CURRENT FILING DATE: 2002-05

```

; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-042-865-107

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Query Match 97.1%; Score 4003; DB 15; Length 722;  
Best Local Similarity 97.2%; Pred. No. 4.6e-264;  
Matches 702: Conservative 4; Mismatches 16; Indels 0

Qy	1	MGRRSALALAW	SALLCQVWSSGVFELKLQEFVNKKGLGNRNCCRGSGPPCACRTFFR	60
Db	1	MGRRSALALAW	SALLCQVWSSGVFELKLQEFVNKKGLGNRNCCRGSGPPCACRTFFR	60
Qy	61	VCLKHQASVS	PEPPCTYGS AVTPVLG VDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS	120
Db	61	VCLKHQASVS	PEPPCTYGS AVTPVLG VDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS	120
Qy	121	LIIEALHTDS	PDDLATENPERLISRLLTQORHLTVGEWSQDLHSSGRTDLRYSYRFPVCDE	180
Db	121	LIIEALHTDS	PDDLATENPERLISRLLTQORHLTVGEWSQDLHSSGRTDLRYSYRFPVCDE	180
Qy	181	HYYGEGCSV	FCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG	240
Db	181	HYYGEGCSV	FCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG	240
Qy	241	ECKRVGWQGRY	CDECIRYPGCVHGTCCQWPWCNCQEGWGLFCNQDLNYCTHHKPCRNG	300
Db	241	ECKRVGWQGRY	CDECIRYPGCVHGTCCQWPWCNCQEGWGLFCNQDLNYCTHHKPCRNG	300
Qy	301	ATCTNTGQGSY	TCSCRPGYTGANCBLEVDECAPSPCKNGASCTDLEDSPSCTCPPGFYGK	360
Db	301	ATCTNTGQGSY	TCSCRPGYTGANCBLEVDECAPSPCKNGASCTDLEDSPSCTCPPGFYGK	360
Qy	361	VCELSAMT	CADGPCFNGGRCSNDPDGGYTCHCPLGFSGFENCEKXMDLCGSSPCSNAGKCV	420
Db	361	VCELSAMT	CADGPCFNGGRCSNDPDGGYTCHCPLGFSGFENCEKXMDLCGSSPCSNAGKCV	420
Qy	421	DLGNSYL	CRCAQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGTYGKNCSAP	480
Db	421	DLGNSYL	CRCAQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGTYGKNCSAP	480
Qy	481	VSRCEHAP	CHNGATCHQRGORYMCECAQGYGGPNCQFLLPEPPPGPMVVLDLSERHMESQ	540
Db	481	VSRCEHAP	CHNGATCHQRGORYMCECAQGYGGPNCQFLLPEPPPGPMVVLDLSERHMESQ	540
Qy	541	GPFPVAV	CAGWLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQREK	600
Db	541	GPFPVAV	CAGWLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQREK	600
Qy	601	DVSVSI	IGATQIKNTNKKADFHGDHGAEKSSFVRYPTVDYNLVRDLKGDEATVRDTHSK	660
Db	601	DVSVSI	IGATQIKNTNKKADFHGDHGAEKSSFVRYPTVDYNLVRDLKGDEATVRDTHSK	660
Qy	661	RDTKCQS	QSLOEKRRSPQHLGVGRFLENTENRPESVYSTSKOTKYQSVYVLSAEKDECVIAT	720
Db	661	RDTKCQS	QSLOEKRRSPQHLGVGRFLENTENRPESVYSTSKOTKYQSVYVLSAEKDECVIAT	720
Qy	721	EV	722	
Db	721	EV	722	



```
RESULT 4
US-10-731-741-4
; Sequence 4, Application US/10731741
; Publication No. US20040171148A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt, Thomas M.
; APPLICANT: Zuniga-Pflucker, Juan-Carlos
; TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell
; TITLE OF INVENTION: Lineage and Methods of Making and Using Them
; FILE REFERENCE: 2223-171
; CURRENT APPLICATION NUMBER: US/10/731,741
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432,525
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-731-741-4

Query Match      97.1%; Score 4003; DB 16; Length 722;
Best Local Similarity 97.2%; Pred. No. 4.6e-264;
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGRSALALAVVSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60
   |||||||
Db 1 MGRSALALAVVSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60

Qy 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 120
   |||||||
Db 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 120

Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCDE 180
   |||||||
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCDE 180

Qy 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240
   |||||||
Db 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240

Qy 241 ECKCRVWQGRYCYDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300
   |||||||
Db 241 ECKCRVWQGRYCYDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300

Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPPGFYGK 360
   |||||||
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPPGFYGK 360

Qy 361 VCELSAMTCADGPGCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420
   |||||||
Db 361 VCELSAMTCADGPGCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420

Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGNKCSAP 480
   |||||||
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGNKCSAP 480

Qy 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQCFLPBPFGPMVVDLSERHMSQG 540
   |||||||
Db 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQCFLPBPFGPMVVDLSERHMSQG 540

Qy 541 GPFPWAVCAGVVLVLLLLLGCAAVVVVCVRLKLQKHQPPPCGGGETETMNNLANCQREK 600
   |||||||
Db 541 GPFPWAVCAGVVLVLLLLLGCAAVVVVCVRLKLQKHQPPPCGGGETETMNNLANCQREK 600

Qy 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660
   |||||||
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660

Qy 661 RDTKCOSQLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
   |||||||
Db 661 RDTKCOSQSAGEEKIAPTLLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
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```
Qy 721 EV 722
   ||
Db 721 EV 722

RESULT 5
US-10-417-719-4
; Sequence 4, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-417-719-4

Query Match      96.4%; Score 3971; DB 14; Length 720;
Best Local Similarity 97.0%; Pred. No. 6.9e-262;
Matches 700; Conservative 4; Mismatches 16; Indels 2; Gaps 2;

Qy 1 MGRSALALAVVSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60
   |||||||
Db 1 MGRSALALAVVSALLCQVSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60

Qy 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 120
   |||||||
Db 61 VCLKH-QASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 119

Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCDE 180
   |||||||
Db 120 LIIEALHTDSPDDLATENPERLISRLTTQRH-TVGEEWSQDLHSSGRTDLRYSYRFVCDE 178

Qy 181 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240
   |||||||
Db 179 HYYGEGSVFCRPRDDAFGHFTCGDRGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG 238

Qy 241 ECKCRVWQGRYCYDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300
   |||||||
Db 239 ECKCRVWQGRYCYDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 298

Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPPGFYGK 360
   |||||||
Db 299 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPPGFYGK 358

Qy 361 VCELSAMTCADGPGCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420
   |||||||
Db 359 VCELSAMTCADGPGCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 418

Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGNKCSAP 480
   |||||||
Db 419 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGNKCSAP 478

Qy 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQCFLPBPFGPMVVDLSERHMSQG 540
   |||||||
Db 479 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQCFLPBPFGPMVVDLSERHMSQG 538

Qy 541 GPFPWAVCAGVVLVLLLLLGCAAVVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQREK 600
```



Db 539 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANCQREK 598  
Qy 601 DVSVSIIGATQIKNTNKKADPHGDHGAEKSSFVKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Db 599 DVSVSIIGATQIKNTNKKADPHGDHGAKKSSFVKVRYPTVDYNLVRDLKGDEATVRDTHSK 658  
Qy 661 RDTKCQSLSQEKRRSPQHGLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Db 659 RDTKCQSSAGEEKIAPTIRGGEIIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 718  
Qy 721 EV 722  
Db 719 EV 720

RESULT 6  
US-10-042-865-108  
; Sequence 108, Application US/10042865  
; Publication No. US20040029216A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Li, Li  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Patturajan, Meera  
; APPLICANT: vernet, Corine A.M  
; APPLICANT: Taylor, Sarah  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Miller, Charles E  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Boldog, Ference L  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Rothenberg, Mark E  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John  
; APPLICANT: Smithson, Glennnda  
; APPLICANT: Gunther, Erik  
; APPLICANT: Stone, David  
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
; TITLE OF INVENTION: Using the Same  
; FILE REFERENCE: 21402-537  
; CURRENT APPLICATION NUMBER: US/10/042,865  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/260,417  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: 60/260,831  
; PRIOR FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: 60/272,338  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/274,876  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/284,704  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 264  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 108  
; LENGTH: 714  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-042-865-108

Query Match 93.4%; Score 3848; DB 15; Length 714;  
Best Local Similarity 93.2%; Pred. No. 1.6e-253;  
Matches 673; Conservative 13; Mismatches 28; Indels 8; Gaps 1;  
Qy 1 MGRRSALALAVVSALLCQWSSGVFELKLOEFVNKGLLGNRNCCRGSGGPPCACRTFFR 60  
Db 1 MGRRSALALAVVSALLCQWSSGVFELKLOEFVNKGLLGNRNCCRGSGGPPCACRTFFR 60  
Qy 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS 120  
Db 61 VCLKHYQASVSPEPPCTYGSAVTAVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS 120  
Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
Qy 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPWKGQOYCTDPICLPGCDDOHGYCDKPG 240  
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGERGEKMDPFGWKGOYCTDPICLPGCDDOHGYCDKPG 240  
Qy 241 ECKRVGWQGRYCDDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
Db 241 ECKRVGWQGRYCDDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
Qy 301 ATCTNTGQSYTCSRPGYTGANCELEVBECAPSPCKNGASCTDLEDSFSTCTPPGFYGK 360  
Db 301 ATCTNTGQSYTCSRPGYTGANCELEVBECAPSPCRNGGSCDLEDSYSTCTPPGFYGK 360  
Qy 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKCV 420  
Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSPCSNGAKCV 420  
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP 480  
Db 421 DLGNSYLCRCQTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGRNCAP 480  
Qy 481 VSRCEHAPCHNGATQHQRQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 540  
Db 481 VSRCEHAPCHNGATQHQRQRYMCECAQGYGGANCQFLLPEPPPDLLVA-----AQG 532  
Qy 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGTETMNNLANCQREK 600  
Db 533 GSFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPDPCGGTETMNNLANCQREK 592  
Qy 601 DVSVSIIGATQIKNTNKKADPHGDHGAEKSSFVKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Db 593 DVSVSIIGATQIKNTNKKADPHGDHGAADKSSFKARYPTVDYNLIRDLKGDEATVRDAHSK 652  
Qy 661 RDTKCQSLSQEKRRSPQHGLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Db 653 RDTKCQSQSVGEKSTSTLRGGEVDPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 712  
Qy 721 EV 722  
Db 713 EV 714  
RESULT 7  
US-10-417-719-5  
; Sequence 5, Application US/10417719  
; Publication No. US20030180784A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF  
; FILE REFERENCE: MBIO1997-002CP2M  
; CURRENT APPLICATION NUMBER: US/10/417,719  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US/09/568,218  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 08/872,855  
; PRIOR FILING DATE: 1997-06-11

; PRIOR APPLICATION NUMBER: 08/832,633									
; PRIOR FILING DATE: 1997-04-04									
; NUMBER OF SEQ ID NOS: 52									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 5									
; LENGTH: 713									
; TYPE: PRT									
; ORGANISM: Rattus No. US20030180784A1vegicus									
US-10-417-719-5									
Query Match 93.2%; Score 3840.5; DB 14; Length 713;									
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QY	61	VCLKHYQASVSPPECTYGSVATPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS	120						
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QY	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE	180						
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRH-TVGEWSQDLHSSGRTDLRYSYRFVUDE	179						
QY	181	HYEGGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKQGYCTDPICLPGCDDQHGYCDKPG	240						
Db	180	HYEGGCSVFCRPRDDAFGHFTCGERGEKMDPGWKQGYCTDPICLPGCDDQHGYCDKPG	239						
QY	241	ECKCRVWQGRYCDICIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG	300						
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QY	301	ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCTCPPGYGK	360						
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QY	361	VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV	420						
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Db	480	VSRCEHAPCHNGATCHQRGQRYMCECAQYGGANCFLLPEPPPDLIIVA-----AQG	531						
QY	541	GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPCGGETETMNNLANCQREK	600						
Db	532	GSFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPDPCCGETETMNNLANCQREK	591						
QY	601	DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK	660						
Db	592	DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLIRDLKGDEATVRDAHSK	651						
QY	661	RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVIAT	720						
Db	652	RDTKCQSQSAGEEKSTSLRGGEVPDRKRPEVYSTSKDTKYQSVVLSAEKDECVIAT	711						
QY	721	EV 722							
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; Sequence 21, Application US/09828366									
; Patent No. US20020010137A1									
; GENERAL INFORMATION:									
; APPLICANT: Genentech, Inc.									

; APPLICANT: Ashkenazi, Avi									
; APPLICANT: Goddard, Audrey									
; APPLICANT: Gurney, Austin L.									
; APPLICANT: Klein, Robert D.									
; APPLICANT: Napier, Mary									
; APPLICANT: Wood, William I.									
; APPLICANT: Yuan, Jean									
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC									
; TITLE OF INVENTION: CELL GROWTH									
; FILE REFERENCE: P1694R1C1									
; CURRENT APPLICATION NUMBER: US/09/828,366									
; CURRENT FILING DATE: 2001-04-05									
; Prior filing data removed - refer to PALM or file wrapper									
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; SEQ ID NO 21									
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; TYPE: PRT									
; ORGANISM: Homo Sapien									
US-09-828-366-21									
Query Match 88.8%; Score 3659.5; DB 9; Length 723;									
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QY	60	RVCLKHYQASVSPPECTYGSVATPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTF	119						
Db	61	RVCLKHYQASVSPPECTYGSVATPVLGVDSFSLPDGGGADSAFNSPIRFPFGFTWPGTF	120						
QY	120	SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD	179						
Db	121	SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD	180						
QY	180	EHYEGGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKQGYCTDPICLPGCDDQHGYCDKP	239						
Db	181	EHYEGGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP	240						
QY	240	GECKCRVWQGRYCDICIRYPGCVHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN	299						
Db	241	GECKCRVWQGRYCDICIRYPGCLHGTCCQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN	300						
QY	300	GATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCTCPPGFYG	359						
Db	301	GATCTNTGQGSYTCSCRPGYTGATCELGIDECDFSPCKNGGSCTDLENSYSCTCPGGFYG	360						
QY	360	KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKAC	419						
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QY	420	VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA	479						
Db	421	VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSCTCPGGYTGRNCSA	480						
QY	480	PVSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCFLLPEPPPGPMVVDLSEKHMESQ	539						
Db	481	PVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCFLLPELPPGPAVVDLLEK-LEQG	539						
QY	540	GGFPFWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCORE	599						
Db	540	GGFPFWAVCAGVILVLMJLLGCAAVVVCVRLRLQKHRRPPADPCRGETETMNNLANCORE	599						
QY	600	KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS	659						
Db	600	KDISYSIIIGATQIKNTNKKADFHGDHSAKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS	659						
QY	660	KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVI	718						
Db	660	KRDTKCQPQGSSEGEKSTPTTLRGGEASERKRPDSCSTSKDTKYQSVYVISEKDECVI	719						
QY	719	ATEV 722							

Db	720 ATEV 723		
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RESULT 9			
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; Sequence 9, Application US/09995593A			
; Patent No. US20020128197A1			
; GENERAL INFORMATION:			
; APPLICANT: SAKANO, SEIJI			
; APPLICANT: ITOH, AKIRA			
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE			
; FILE REFERENCE: KP8447DIV			
; CURRENT APPLICATION NUMBER: US/09/995,593A			
; CURRENT FILING DATE: 2002-02-28			
; PRIOR APPLICATION NUMBER: 09/068,740			
; PRIOR FILING DATE: 1998-06-18			
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; PRIOR APPLICATION NUMBER: JP 7-311811			
; PRIOR FILING DATE: 1995-11-30			
; PRIOR APPLICATION NUMBER: PCT/JP96/03356			
; PRIOR FILING DATE: 1996-11-15			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 9			
; LENGTH: 723			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
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Best Local Similarity 87.0%; Pred. No. 1.1e-240;			
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;			
Qy	1	MGRRSALALAVVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCCRGSG-PPCACRTFF	59
Db	1	MGSRCALALAVLSALLCQWSSGVFELKLOEFVNKKGLLGNRNCCRGAGPPCACRTFF	60
Qy	60	RVCLKHQASVSEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTF	119
Db	61	RVCLKHQASVSEPPCTYGSVTPVLGVDSFSLPDGGADSAFNSPIRFPFGFTWPGTF	120
Qy	120	SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD	179
Db	121	SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD	180
Qy	180	EHYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGOYCTDPICLPGCDDQHGCDKP	239
Db	181	EHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP	240
Qy	240	GECKRVGMQGRYCDDECIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCRN	299
Db	241	GECKRVGMQGRYCDDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCKN	300
Qy	300	GATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSPSCTCPPGFYG	359
Db	301	GATCTNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYG	360
Qy	360	KVCELSAMTCADGPCFNGGRCSNDPDDGGYTCHCPLGFSGFNCEKKMDLCSSSPCSNGAKC	419
Db	361	KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC	420
Qy	420	VDLGNLSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA	479
Db	421	VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGRNCSA	480
Qy	480	PVSRCEHAPCHNGATCHQRQRYMCECAQYGGPNQCQLLPEPPPGPMVVDLSERHMESQ	539
Db	481	PVSRCEHAPCHNGATCHERGHRVYCECARGYGGPNQCQLLPELPPGPAVVDLLEK-LEQG	539
Qy	540	GGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPCGGETETMNNLANCQRE	599

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Qy	600	KDVSVSIIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRDLKGDATVRDTHS	659
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Qy	660	KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTKOTKYQSVVYVLSAEKDECVI	718
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; Sequence 346, Application US/10028072			
; Publication No. US20030004311A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang			
; TITLE OF INVENTION:			
; FILE REFERENCE:			
; CURRENT APPLICATION NUMBER: US/10/028,072			
; CURRENT FILING DATE: 2001-12-19			
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; PRIOR FILING DATE: 1998-06-26  
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; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07

Query Match

88.8%; Score 3659.5; DB 14; Length 723;



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Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

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QY 60 RVCLKHYQASVSPPECTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTF 119
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QY 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 179
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QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP 239
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QY 240 GECKCRVWQGRYCDDECIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 299
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QY 300 GATCTNTGQSYTCSRPGYTGANCELEVDDECAPSPCKNGASCTDLEDSEFSCTCPPGFY 359
Db 301 GATCTNTGQSYTCSRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYCTCPPGFY 360

QY 360 KVCELSAMTCADGPCFNGGRCSNDPDDGGYTCHCPLGFSGFNCEKMDLCSGSSPCSNGAKC 419
Db 361 KICELSAMTCADGPCFNGGRCSNDPDDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKC 420

QY 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479
Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGYTGRNCSA 480

QY 480 PVSRCHEAPCHNGATCHQRGORYMCECAQYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 539
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QY 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQRE 599
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QY 600 KDVSVSIIGATQIKNTNKKADFHGDHGAESKFVRYPTVDYNLVRDLKGDEATVRDTHS 659
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Db 660 KRDTKCQPGSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVI 719

QY 719 ATEV 722
Db 720 ATEV 723
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RESULT 11

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US-10-140-808-346
; Sequence 346, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
```

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-346

Query Match 88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

QY 1 MGRSALALAVVSALLCQWSSGVFELKIQEFVNKKGLGNRNCCRGSG-PPCACRTFF 59
Db 1 MGRSALALAVLSALLCQWSSGVFELKIQEFVNKKGLGNRNCCRGAGPPCACRTFF 60

QY 60 RVCLKHYQASVSPPECTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRPFPGFTWPGTF 119
Db 61 RVCLKHYQASVSPPECTYGSVAVTPVLGVDSFSLPDGGGADSAFSPNPIRPFPGFTWPGTF 120

QY 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 179
Db 121 SLIIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCD 180

QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP 239
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240

QY 240 GECKCRVWQGRYCDDECIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 299
Db 241 GECKCRVWQGRYCDDECIRYPGCLHGTCQWPQCNCQEGWGLFCNQDLNYCTHHKPCKN 300

QY 300 GATCTNTGQSYTCSRPGYTGANCELEVDDECAPSPCKNGASCTDLEDSEFSCTCPPGFY 359
Db 301 GATCTNTGQSYTCSRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYCTCPPGFY 360

QY 360 KVCELSAMTCADGPCFNGGRCSNDPDDGGYTCHCPLGFSGFNCEKMDLCSGSSPCSNGAKC 419
Db 361 KICELSAMTCADGPCFNGGRCSNDPDDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKC 420

QY 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479
Db 421 VDLGDAYLCRCQAGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGYTGRNCSA 480

QY 480 PVSRCHEAPCHNGATCHQRGORYMCECAQYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 539
Db 481 PVSRCHEAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTK-LEGQ 539

QY 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGTETMNNLANCQRE 599
Db 540 GGPFPWAVCAGVILVLMLLGCAAVVVCVRLQLQHRPPADPCRGETETMNNLANCQRE 599

QY 600 KDVSVSIIGATQIKNTNKKADFHGDHGAESKFVRYPTVDYNLVRDLKGDEATVRDTHS 659
Db 600 KDISVSIIGATQIKNTNKKADFHGDHSAADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659

QY 660 KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 718
Db 660 KRDTKCQPGSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVI 719

QY 719 ATEV 722
Db 720 ATEV 723
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RESULT 12  
US-10-121-049-346  
; Sequence 346, Application US/10121049  
; Publication No. US2003002239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C17  
; CURRENT APPLICATION NUMBER: US/10/121,049  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-049-346  
  
Query Match 88.8%; Score 3659.5; DB 14; Length 723;  
Best Local Similarity 87.0%; Pred. No. 1.1e-240;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
  
Qy 1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCARTFF 59  
Db 1 MGRSALALAVLSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGAGPPPCARTFF 60  
  
Qy 60 RVCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGGGADSAFNSNPIRFPFGFTWPGTF 120  
  
Qy 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRLHTVGEEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIIEALHTDSPDDLATENPERLISRLATQRLHTVGEEWSQDLHSSGRTDLKYSYRFVCD 180  
  
Qy 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGCDKP 239  
Db 181 EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240  
  
Qy 240 GECKRVGWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCRN 299  
Db 241 GECKRVGWQGRYCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCKN 300  
  
Qy 300 GATCTNTGQSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDVSFCTCPPGFGY 359  
Db 301 GATCTNTGQSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGFGY 360  
  
Qy 360 KVCELSAMTCADGPCFNGGRCSNPDGGYTCCHPLGFSGFNCEKMDLCSSPSCSNGAKC 419  
Db 361 KICELSAMTCADGPCFNGGRCSNPDGGYSRCPCPVGYSGFNCEKKIDYCSSPSCSNGAKC 420  
  
Qy 420 VDLGNSYLRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGKNCSA 480

Qy 480 PVSRCCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMSQ 539  
Db 481 PVSRCCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTK-LEGQ 539  
  
Qy 540 GGPEPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGETETMNNLANCORE 599  
Db 540 GGPEPWAVCAGVILVLLMLLGCAAVVVCVRLQLQKRPADPCRGETETMNNLANCORE 599  
  
Qy 600 KDVSVSIIGATQIKNTNKKADPHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDISVSIIGATQIKNTNKKADPHGDHSDAKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659  
  
Qy 660 KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVYVLSAEKDECVI 718  
Db 660 KRDTKCQPQSGSGEERGTPTTLRGEASERKRPPDSCGSTKDTKYQSVYVISEEKDECVI 719  
  
Qy 719 ATEV 722  
Db 720 ATEV 723  
  
RESULT 13  
US-10-123-904-346  
; Sequence 346, Application US/10123904  
; Publication No. US20030022328A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C54  
; CURRENT APPLICATION NUMBER: US/10/123,904  
; CURRENT FILING DATE: 2002-04-16  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-123-904-346  
  
Query Match 88.8%; Score 3659.5; DB 14; Length 723;  
Best Local Similarity 87.0%; Pred. No. 1.1e-240;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
  
Qy 1 MGRSALALAVVSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGSG-PPCARTFF 59  
Db 1 MGRSALALAVLSALLCQVWSSGVFELKLOEFVNKKGLGNRNCRRGGAGPPPCARTFF 60  
  
Qy 60 RVCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGAGIDPAFNSNPIRFPFGFTWPGTF 119  
Db 61 RVCLKHYQASVSPEPPCTYGSVATPVLGVDVSFSLPDGGGADSAFNSNPIRFPFGFTWPGTF 120  
  
Qy 120 SLIIIEALHTDSPDDLATENPERLISRLTTQRLHTVGEEWSQDLHSSGRTDLRYSYRFVCD 179  
Db 121 SLIIIEALHTDSPDDLATENPERLISRLATQRLHTVGEEWSQDLHSSGRTDLKYSYRFVCD 180  
  
Qy 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGCDKP 239

Db 181 EHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240  
Qy 240 GECKCRVWQGRYCDCEIRYPGCVHGTCCQPMQCNQEGWGLFCNQDLNCTHHKPCRN 299  
Db 241 GECKCRVWQGRYCDCEIRYPGCLHGTCCQPMQCNQEGWGLFCNQDLNCTHHKPCKN 300  
Qy 300 GATCTNTGQSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTPPGFY 359  
Db 301 GATCTNTGQSYTCSCRPGYTGATCELGIDEDCPSPCKNGGSCDLENSYSCTCPPGFY 360  
Qy 360 KVCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKC 419  
Db 361 KICELSAMTCADGPCFNGRCSDSPDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKC 420  
Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCCTCPPGTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNDNVDDCASSPCANGGTCRDGVNDFSCCTCPPGTGRNCSA 480  
Qy 480 PVSRCCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPPGMVVDLSERHMESQ 539  
Db 481 PVSRCCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTK-LEGQ 539  
Qy 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGGETETMNNLANCQRE 599  
Db 540 GGPFPWAVCAGVILVLMLLGCAAVVVCVRLRLQKHRRPPADPCRGETETMNNLANCQRE 599  
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDISYSIIIGATQIKNTNKKADFHGDHSAKNGFKARYPAVDYNLVQDLKGGDDTAVRDAHS 659  
Qy 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVI 718  
Db 660 KRDTKCQPGQSSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVI 719  
Qy 719 ATEV 722  
Db 720 ATEV 723

RESULT 14  
US-10-140-470-346

; Sequence 346, Application US/10140470  
; Publication No. US20030022331A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C160  
; CURRENT APPLICATION NUMBER: US/10/140,470  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-140-470-346  
Query Match 88.8%; Score 3659.5; DB 14; Length 723;  
Best Local Similarity 87.0%; Pred. No. 1.1e-240;  
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;  
Qy 1 MGRRSALALAVVSALLCQWSSGVFELKQEFVNKKGLLGNRNCCRGSG-PPCACRTFF 59  
Db 1 MGSRCALALAVLSALLCQWSSGVFELKQEFVNKKGLLGNRNCCRGAGPPBCACRTFF 60  
Qy 60 RVCLKHYQASVSPPEPTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPRIRPFPGFTWPGTF 119  
Db 61 RVCLKHYQASVSPPEPTYGSAVTPVLGVDSFSLPDGGGADSAFNSNPRIRPFPGFTWPGTF 120  
Qy 120 SLIIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSQDLHSSGRTLRYSYRFVCD 179  
Db 121 SLIIEALHTDSPDDLATENPERLISRLATQRLHDTVGEWSQDLHSSGRTLKYSYRFVCD 180  
Qy 180 EHYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPGWKQYCTDPICLPGCDDQHGFCDKP 239  
Db 181 EHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP 240  
Qy 240 GECKCRVWQGRYCDCEIRYPGCVHGTCCQPMQCNQEGWGLFCNQDLNCTHHKPCRN 299  
Db 241 GECKCRVWQGRYCDCEIRYPGCLHGTCCQPMQCNQEGWGLFCNQDLNCTHHKPCKN 300  
Qy 300 GATCTNTGQSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSFSCCTPPGFY 359  
Db 301 GATCTNTGQSYTCSCRPGYTGATCELGIDEDCPSPCKNGGSCDLENSYSCTCPPGFY 360  
Qy 360 KVCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKC 419  
Db 361 KICELSAMTCADGPCFNGRCSDSPDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKC 420  
Qy 420 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCCTCPPGTGKNCSA 479  
Db 421 VDLGDAYLCRCQAGFSGRHCDNDNVDDCASSPCANGGTCRDGVNDFSCCTCPPGTGRNCSA 480  
Qy 480 PVSRCCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPPGMVVDLSERHMESQ 539  
Db 481 PVSRCCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTK-LEGQ 539  
Qy 540 GGPFPWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGGETETMNNLANCQRE 599  
Db 540 GGPFPWAVCAGVILVLMLLGCAAVVVCVRLRLQKHRRPPADPCRGETETMNNLANCQRE 599  
Qy 600 KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHS 659  
Db 600 KDISYSIIIGATQIKNTNKKADFHGDHSAKNGFKARYPAVDYNLVQDLKGGDDTAVRDAHS 659  
Qy 660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVYVLSAEKDECVI 718  
Db 660 KRDTKCQPGQSSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVI 719  
Qy 719 ATEV 722  
Db 720 ATEV 723  
RESULT 15  
US-10-175-746-346  
; Sequence 346, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C160  
; CURRENT APPLICATION NUMBER: US/10/140,470  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien

```
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-346

Query Match      88.8%; Score 3659.5; DB 14; Length 723;
Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels 3; Gaps 3;

Qy      1  MGRRSALALAWSALLCQVSSGVFELKQEFVNKKGLLGNRNCRRGGSG-PPCACRTFF 59
Db      1  MGSRCALALAVLSALLCQVSSGVFELKQEFVNKKGLLGNRNCRRGGAGPPPCACRTFF 60

Qy      60  RVCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF 119
Db      61  RVCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF 120

Qy      120  SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 179
Db      121  SLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCD 180

Qy      180  EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKQYCTDPICLPGCDDQHGYCDKP 239
Db      181  EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKPGPYCTEPICLPGCDEQHGFCDKP 240

Qy      240  GECKRVGWQGRYDECIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN 299
Db      241  GECKRVGWQGRYDECIRYPGCLHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300

Qy      300  GATCNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSEFSCCTCPGFGY 359
Db      301  GATCNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGSCTDLENSYSCTCPGFGY 360

Qy      360  KVCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPSCNGAKC 419
Db      361  KICELSAMTCADGPCFNGGRCSNPDGGYSRCPPVGYSGFNCEKKIDYCSSSPSCNGAKC 420

Qy      420  VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGTYGKNCSA 479
Db      421  VDLGDAYLCRCQAGFSGRHCDNVDNDDCASSPCANGGTCRDGVNDFSCTCPGTYGRNCSA 480

Qy      480  PVSRCHEAPCHNGATCHQRGQRYMCECAQGYGPNQCFLLEPPPPGPMVVDLSEHNMESQ 539
Db      481  PVSRCHEAPCHNGATCHERHRYVCECARGYGGPNQCFLLELPFGPAVVDLJEK-LEGQ 539

Qy      540  GGPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGETETMNNLANCORE 599
Db      540  GGPFPPWAVCAGVILVLLMLLLGCAAVVVCVRLRLQKHRRPADPCRGETETMNNLANCORE 599

Qy      600  KDVSYSIIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
Db      600  KDISYSIIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS 659

Qy      660  KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVVLSAEKDECVI 718
Db      660  KRDTKQCPQGSSGEEKGTPTTLRGGEASERKRDPDGGCSTSKDTKYQSVYVISEEKDECVI 719
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Qy 719 ATEV 722  
Db 720 ATEV 723

Search completed: November 29, 2004, 13:42:00  
Job time : 74.7322 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 18.0943 Seconds  
(without alignments)  
3839.238 Million cell updates/sec

Title: US-09-783-931-12  
Perfect score: 4121  
Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4003	97.1	722	2 I48324	DELTA-like 1 - mou
2	3368	81.7	728	2 I50719	C-Delta-1 - chicke
3	1879.5	45.6	685	2 JC7570	Delta-4 protein -
4	1828	44.4	686	2 JC7569	Delta-4 protein -
5	1468.5	35.6	833	2 S19087	gene Delta protein
6	1463.5	35.5	832	2 A31246	neurogenic protein
7	1463.5	35.5	880	2 S00670	neurogenic repetit
8	1312	31.8	1220	2 A56136	jagged protein pre
9	1130	27.4	1408	2 S16148	gene serrate prote
10	810	19.7	2524	2 A35844	Xotch protein - Af
11	807.5	19.6	2531	2 A46019	notch-1 protein -
12	794.5	19.3	2531	2 S18188	notch protein homo
13	771	18.7	1064	2 A40136	fibropellin Ia - s
14	765.5	18.6	2437	2 S42612	transmembrane prot
15	761	18.5	1203	2 A49175	Motch B protein -
16	761	18.5	2471	2 A49128	cell-fate determin
17	759	18.4	2555	2 A40043	notch protein homo
18	756	18.3	2352	2 T30201	Notch homolog prot
19	753	18.3	2531	2 T31070	Notch homolog - se
20	747	18.1	2321	2 S78549	notch3 protein - h
21	747	18.1	2703	1 A24420	notch protein - fr
22	742	18.0	2318	2 S45306	notch 3 protein -
23	711	17.3	2139	2 A35672	crumbs protein - f
24	702.5	17.0	1964	2 T09059	notch4 - mouse
25	698	16.9	861	2 A48825	Notch homolog Motc
26	682	16.5	570	2 A48836	fibropellin C prec
27	632	15.3	1372	2 T25933	hypothetical prote
28	628	15.2	385	2 S53718	homeotic protein d
29	623	15.1	473	2 A56175	adhesive plaque pr

30	621.5	15.1	385	2 A54785	preadipocyte facto
31	601.5	14.6	1429	2 S06434	homeotic protein 1
32	596	14.5	383	2 S53716	delta-like homeoti
33	578.5	14.0	1295	2 A32901	glp1 protein precu
34	570.5	13.8	1469	2 B36665	slit protein 2 pre
35	570.5	13.8	1480	2 A36665	slit protein 1 pre
36	567	13.8	1531	2 T42218	slit-1 protein hom
37	566	13.7	1722	2 E89753	protein FilC7.4 [i
38	550.5	13.4	308	2 JC7125	epidermal growth f
39	538	13.1	601	2 T22025	hypothetical prote
40	538	13.1	601	2 D89711	protein F40E10.4 [
41	535	13.0	1687	2 T30176	EGF repeat transme
42	519.5	12.6	1025	2 T42626	secreted leucine-r
43	511.5	12.4	1523	2 T13953	MEGF5 protein - ra
44	489	11.9	387	2 B49175	Motch A protein -
45	462	11.2	3623	2 T08618	intrinsic factor-B

ALIGNMENTS

RESULT 1  
I48324

DELTA-like 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48324

R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.

Development 121, 2407-2418, 1995

A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin

A;Reference number: I48324; MUID:95401858; PMID:7671806

A;Accession: I48324

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-722 <RES>

A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065

C;Genetics:

A;Gene: Dll1

C;Superfamily: delta-4 protein; EGF homology

F;331-362/Domain: EGF homology <EGF2>

F;446-477/Domain: EGF homology <EGF>

F;484-515/Domain: EGF homology <EGF1>

Query Match 97.1%; Score 4003; DB 2; Length 722;  
Best Local Similarity 97.2%; Pred. No. 1.1e-240;  
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVFNKKGLLGNRNCRRGGSGPPCACRTFFR 60

Db 1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVFNKKGLLGNRNCRRGGSGPPCACRTFFR 60

QY 61 VCLKHYQASVSEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGTWPGTFS 120

Db 61 VCLKHYQASVSEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGTWPGTFS 120

QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRLTLVGEWSQDLHSSGRTDLRYSYRFVVCDE 180

Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRLTLVGEWSQDLHSSGRTDLRYSYRFVVCDE 180

QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPGWKGOYCTDPICLPGCDDQHGVCCKPG 240

Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPGWKGOYCTDPICLPGCDDQHGVCCKPG 240

QY 241 ECKCRVGMQGRYCDDECIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCRNG 300

Db 241 ECKCRVGMQGRYCDDECIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCRNG 300

QY 301 ATCTNTGGSYTCSCRPGYTGANCELEVBECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360

Db 301 ATCTNTGGSYTCSCRPGYTGANCELEVBECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360

QY 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFENCEKMDLCGSSPCSNAGKCV 420

|||||

Db 361 VCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCEKMDLCGSSPCSNCAKCV 420  
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCsap 480  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCsap 480  
Qy 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNQCQLLPEPPPGPMVVDLSERHMESQG 540  
Db 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNQCQLLPEPPPGPMVVDLSERHMESQG 540  
Qy 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK 600  
Db 541 GPPFWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK 600  
Qy 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Qy 661 RDTKCQSLSQLEKRRSPQHILGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Db 661 RDTKCQSLSQLEKRRSPQHILGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
Qy 721 EV 722  
Db 721 EV 722

RESULT 2  
I50719  
C-Delta-1 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50719  
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.  
Nature 375, 787-790, 1995  
A;Title: Expression of a Delta homologue in prospective neurons in the chick.  
A;Reference number: I50719; MUID:95319507; PMID:7596411  
A;Accession: I50719  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-728 <HEN>  
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g8824  
C;Superfamily: delta-4 protein; EGF homology  
F;299-332/Domain: EGF homology <EGX1>  
F;339-370/Domain: EGF homology <EGF1>  
F;416-447/Domain: EGF homology <EGX2>  
F;454-485/Domain: EGF homology <EGF>  
F;492-523/Domain: EGF homology <EGF3>

Query Match 81.7%; Score 3368; DB 2; Length 728;  
Best Local Similarity 78.5%; Pred. No. 2.4e-201;  
Matches 574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;

Qy 1 MGRSALALAVVSALL--CQWSSGVFELKLQEFVNKKGLLGNRNCCRGSGP-----P 52  
Db 1 MGRFLLTLALLSALLCRCQVDCSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGQQQ 59  
Qy 53 CACRTFFRVCLKHQYQASVSPPEPCTYGSVTPVLGVDSFSLPDGA-GIDPAFSNPIRFPF 111  
Db 60 CDCKTFFRVCLKHQYQASVSPPEPCTYGSAITPVLGANSFSPVDGAGGADPAFSNPIRFPF 119  
Qy 112 GFTWPGTFSLLIEALHTDSPDDLATENPERLISRLTTORHLTVGEEWSQDLHSSGRTDLR 171  
Db 120 GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLK 179  
Qy 172 YSRFVCDHEHYGEGCSVFRCPRDDAFGHFTCGDRGEMCDPGWKGYCTDPICLPGCDD 231  
Db 180 YSRFVCDHEHYGEGCSVFRCPRDDRFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDE 239  
Qy 232 QHGYCDKPGECKRVGWQGRYCDICIRYPGCVHGTCCQQPQCNCQEGWGGLFCNQDLNYC 291  
Db 240 QHGYCDKPGECKRVGWQGRYCDICIRYPGCLHGTCCQQPQCNCQEGWGGLFCNQDLNYC 299

Qy 292 THHKPCRNATCTNTGQSYTCSRPGYTGANCELEBDECAPSPCKNGASCTDLEDSFSC 351  
Db 300 THHKPCKNATCTNTGQSYTCSRPGYTSSSCEIBEINECDANPCKNGSGCTDLENSYSC 359  
Qy 352 TCPPGFYGKVCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFGFNCEKMDLCGSS 411  
Db 360 TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNDPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419  
Qy 412 PCSNGAKCVDLGN SYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPG 471  
Db 420 PCANGAQCVDLGN SYICQCQAGFTGRHCDDNVDDCASFPVNGGTCQDGVNDYSCTCPG 479  
Qy 472 YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNQCQLLPEPPPGPMVVDL 531  
Db 480 YNGKNCSTPVSRCENPCHNGATCHERSNRYVCECARGYGGNLNCQFLLEPPPPQGPVIVDF 539  
Qy 532 SERHMESQGGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMN 591  
Db 540 TEKYTEGQNSQFPWIAVCAGIILVLMLLGCAAVVVCVRLKVQKRHHQPEACRSETETMN 599  
Qy 592 NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFVKRYPTVDYNLVRDLKGDE 651  
Db 600 NLANCQREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKRYPSVDYNLVHELK-NE 657  
Qy 652 ATVRDTHSKRDTKCQSLSQLEKRRSPQHILGVGRFLTENRPESVYSTSKDTKYQSVYVLSA 711  
Db 658 DSVKEHKGCEAKCETYDSEAEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 717  
Qy 712 EKDECVIATEV 722  
Db 718 EKDECIATEV 728

RESULT 3  
JC7570  
Delta-4 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: JC7570  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J.  
Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.  
A;Reference number: JC7569; MUID: 21064937; PMID:11134954  
A;Accession: JC7570  
A;Molecule type: mRNA  
A;Residues: 1-685 <YON>  
A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894  
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane rec  
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.  
C;Genetics:  
A;Gene: delta-4  
C;Superfamily: delta-4 protein; EGF homology  
C;Keywords: transmembrane protein

Query Match 45.6%; Score 1879.5; DB 2; Length 685;  
Best Local Similarity 48.6%; Pred. No. 3.7e-109;  
Matches 363; Conservative 99; Mismatches 190; Indels 95; Gaps 23;

Qy 4 RSALALAVVSALLCQVW-----SSGVFELKLQEFVNKKGLLGNRNCCRGSGGPC--ACR 56  
Db 6 RSASGWALL--LLVALMQQRAAGSGVFQLQLEFINERGVL-----ASGRPCEPGCR 55  
Qy 57 TFFRVCLKHQYQASVSPPEPCTYGSVTPVLGVDSFSLPD---GAGIDPAFSNPIRFPFGF 113  
Db 56 TFFRVCLKHFAQVVPSP-GECTFGTVSTPVLGTNSFAVRDDSSGGG-----RNPLQLPFPNF 109  
Qy 114 TWPGTFSLLIEALHTDSPDDLATE--NPERLISRLTTORHLTVGEEWSQDLHSSGRTDLR 171  
Db 110 TWPGTFSLLIEAWHAPG-DDLRPEALPPDALISKIAIQGSLAVGQNWLLEDQETSTLTRLR 168  
Qy 172 YSRFVCDHEHYGEGCSVFRCPRDDAFGHFTCGDRGEMKCDPGWKGYCTDPICLPGCDD 231  
Db 169 YSRVICSDNYYGDNCSRLCKKRNDFHGHYVVCQPDGNLSCLPGWTGEYCCQPICLSGCHE 228





Qy	61	VCLKHYQASVSEPPCTYGSATVPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTF	119
Db	67	VCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDARQFQNGKFTNPIQFPFSFSGTF	126
Qy	120	SLIIEALHTDSPDDLATENPERLISRLLTQRLHLLTVGEEMSQDLHSSGRTDLRYSYRFVCD	179
Db	127	SLIIEAWHDTNNSGNARTN-KLLIQRLLVQQVLEVSSEWKNKSESYTSLEYDFRVTC	185
Qy	180	EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKGYCTDPICLPGCDDQHGYCDKP	239
Db	186	LNYYGSGCAKFCRPRDSDFGHSTCSETGEIICLTGWQGDYCHIPKCAKGC--EHGHC	243
Qy	240	GECKRVGWQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN	299
Db	244	NQVCQLGWKGALCNECVLEPNCIHGTCNKPWTICINEGWGGLYCNQDLNYCTNHRPCKN	303
Qy	300	GATCTNTGQGSYTCSCRPGYTGANCELEVDECAP--SPCKNGASCTD---LEDSFSCTCP	354
Db	304	GGTCFNTGEGLYTCKAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPTHKTGYKCHCA	363
Qy	355	PGFYGKVCELSAMTCADGPCFNGGRCSNDPDG-----GYTCHCPLGFSGFNCEKMDLC	408
Db	364	NGWSGKMCCEKVLTCSDKPC-HQGICRNVRPGLSGKGGYQCECPIGYSGPNCDLQDNC	422
Qy	409	GSSP-----CSNGAKCVDLGNLYLCRCQAG	433
Db	423	SPNPCINGGSCQPSGKCIAPGSGTRCETNIDDLGHQCENGGTCIDMVNQYRCQCPVG	482
Qy	434	FSGRYCEDNVDDCASSPCANGGTCRDSVNDFSTCTPPGYTGKNCSAPVSRCEHAPCHNGA	493
Db	483	FHGTHCSSKVDLCLIRPCANGGTCNLNNDYQCTCRAGFTGKDCSVDIDECSSGPGCHNGG	542
Qy	494	TCHQRGQRYMCECAQGYGGPNCQFLLEPPPPGPMVVDLSERHMESQGG-----	541
Db	543	TCMNRVNSFECVCANGFRGKQCD---EESYDSVTFDAHQYGATTQARADGLTNAQVVLI	598
Qy	542	-----PPFWAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANC	596
Db	599	AVFSVAMPLVAVIA-----ACVVFCKMRKRKRAQEKDDAEARKQNEQNAVATM	646
Qy	597	QRE-KDVSYSIIIGATQIKNTNKKADFHGDHG	626
Db	647	HHNGSGVGVALASASLGKGTGSNSGLTFDGG	677
RESULT 6			
A31246			
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)			
C;Species: Drosophila melanogaster			
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002			
C;Accession: A31246			
R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T. Genes Dev. 2, 1723-1735, 1988			
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a			
A;Reference number: A31246; MUID:89196890; PMID:3149249			
A;Accession: A31246			
A;Molecule type: mRNA			
A;Residues: 1-832 <KOP>			
A;Cross-references: GB:Y00222			
C;Genetics:			
A;Gene: FlyBase:D1			
A;Cross-references: FlyBase:FBgn0000463			
C;Superfamily: neurogenic protein delta; EGF homology			
F;295-328/Domain: EGF homology <EGX1>			
F;422-450/Domain: EGF homology <EGF1>			
F;457-488/Domain: EGF homology <EGF>			
F;533-564/Domain: EGF homology <EGF3>			
Query Match 35.5%; Score 1463.5; DB 2; Length 832;			
Best Local Similarity 40.2%; Pred. No. 2.6e-83;			
Matches 273; Conservative 95; Mismatches 240; Indels 71; Gaps 14;			
Qy	11	VVSALLC-----QWSSGVFELKLQEFVNKKGLGNRNCCRG---GSGPPC--ACRTFFR	60

Db	7	LTAPICFTVIVQHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATKCLGSCKTRFR	66
Qy	61	VCLKHYQASVSEPPCTYGSATVPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTF	119
Db	67	VCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDARQFQNGKFTNPIQFPFSFSGTF	126
Qy	120	SLIIEALHTDSPDDLATENPERLISRLLTQRLHLLTVGEEMSQDLHSSGRTDLRYSYRFVCD	179
Db	127	SLIIEAWHDTNNSGNARTN-KLLIQRLLVQQVLEVSSEWKNKSESYTSLEYDFRVTC	185
Qy	180	EHYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKGYCTDPICLPGCDDQHGYCDKP	239
Db	186	LNYYGSGCAKFCRPRDSDFGHSTCSETGEIICLTGWQGDYCHIPKCAKGC--EHGHC	243
Qy	240	GECKRVGWQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN	299
Db	244	NQVCQLGWKGALCNECVLEPNCIHGTCNKPWTICINEGWGGLYCNQDLNYCTNHRPCKN	303
Qy	300	GATCTNTGQGSYTCSCRPGYTGANCELEVDECAP--SPCKNGASCTD---LEDSFSCTCP	354
Db	304	GGTCFNTGEGLYTCKAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPTHKTGYKCHCR	363
Qy	355	PGFYGKVCELSAMTCADGPCFNGGRCSNDPDG-----GYTCHCPLGFSGFNCEKMDLC	408
Db	364	NGWSGKMCCEKVLTCSDKPC-HQGICRNVRPGLSGKGGYQCECPIGYSGPNCDLQDNC	422
Qy	409	GSSP-----CSNGAKCVDLGNLYLCRCQAG	433
Db	423	SPNPCINGGSCQPSGKCIAPGSGTRCETNIDDLGHQCENGGTCIDMVNQYRCQCPVG	482
Qy	434	FSGRYCEDNVDDCASSPCANGGTCRDSVNDFSTCTCPGYTGKNCSAPVSRCEHAPCHNGA	493
Db	483	FHGTHCSSKVDLCLIRPCANGGTCNLNNDYQCTCRAGFTGKDCSVDIDECSSGPGCHNGG	542
Qy	494	TCHQRGQRYMCECAQGYGGPNCQFLLEPPPPGPMVVDLSERHMESQG-----GPFPWAV	548
Db	543	TCMNRVNSFECVCANGFRGKQCD---EESYDSVTFDAHQYGATTQARADGLANAQVVLI	598
Qy	549	CAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGTETMNNLANCQRE-KDVSYSII	607
Db	599	AVFSVAMPLVAVIAACVVFCKMRKRKRAQEKDNEARKQNEQNAVATMHHNGSAVGVALA	658
Qy	608	GATQIKNTNKKADFHGDHG	626
Db	659	SASMGKGTGSNSGLTFDGG	677
RESULT 7			
S00670			
neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)			
N;Alternate names: gene D1 protein			
C;Species: Drosophila melanogaster			
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004			
C;Accession: S00670; A26637			
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A. EMBO J. 6, 3431-3440, 1987			
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic			
A;Reference number: S00670			
A;Accession: S00670			
A;Molecule type: mRNA			
A;Residues: 1-880 <VAE>			
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:g7852; PID:g7853			
R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ort			
EMBO J. 6, 761-766, 1987			
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t			
A;Reference number: A91081; MUID:87218537; PMID:3107986			
A;Accession: A26637			
A;Molecule type: mRNA			
A;Residues: 422-436,'ET',439-458,'A',460-489,'T',491-621 <KNU>			
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563			
C;Genetics:			
A;Gene: Delta; D1			



A;Cross-references: FlyBase:FBgn0000463  
C;Superfamily: neurogenic protein delta; EGF homology  
C;Keywords: transmembrane protein  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>  
F;457-488/Domain: EGF homology <EGF1>  
F;533-564/Domain: EGF homology <EGF2>

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Query Match      35.5%; Score 1463.5; DB 2; Length 880;
Best Local Similarity 40.2%; Pred. No. 2.7e-83;
Matches 273; Conservative 95; Mismatches 240; Indels 71; Gaps 14;

QY 11 VVSALLC-----QVWSSGVFELKLQEFVNKKGLLGNRNCCRG---GSGPPC--ACRTFFR 60
Db 7 LLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCSSGESDGATKCLGSKTRFR 66

QY 61 VCLKHYQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGAGI-DPAFSPNPIRFPFGFTWPGTF 119
Db 67 LCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDQORFQNKGFNTPIQFPFSFWPGTF 126

QY 120 SLIIEALHTDSPDDLATENPERLISRLLTQRHLTVGEWSQDLHSSGRTDLRYSRFVCD 179
Db 127 SLIVEAWHDTNNSGNARTN-KLLIQRLLVQVLEVSSEWKTNKSQYTSLEYDFRVTC 185

QY 180 EHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGYCTDPICLPGCDDOHGYCDKP 239
Db 186 LNYYGSGCAKFCRPRDDSPGHSTCSETGEIICLTGWQGDYCHIPKCAKGC--EHGHCDKP 243

QY 240 GECKCRVGWQGRYCDICIRYPCGVHGTCCQPWQCNCQBGWGLFCNQDLNYCTHHKPCRN 299
Db 244 NQCVQLGWKALCNECVLEPNCIHGTCNKPWTCINEGWGGLYCNQDLNYCTNHRPCKN 303

QY 300 GATCTNTGQSYTCSRPGYTGANCELEVDECAP--SPCKNGASCTD---LEDSFSCTCP 354
Db 304 GGTCTNTGEGLYTCKCAPGSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCR 363

QY 355 PGFYGKVCELSAMTCADGPCFNGGRCSDNPDG-----GYTCHCPLGFSGFENCEKKMDLC 408
Db 364 NGWSGKMCEEKVLTCSDKPC-HQICRNVRPGLGSKQGYQCECPIGYSGPNCDLQLDNC 422

QY 409 GSSP-----CSNGAKCVDLGNLYLCRCQAG 433
Db 423 SPNFCINGSCQPSGKCIQPSGFSGTRCETNIDDCILGHQCENGGTCTIDMVNQYRCQVPG 482

QY 434 FSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGA 493
Db 483 FHGTHCSSKVDLCLIRPCANGGTCNLNNDYQCTCRAGFTGKDCSVIDECSSGPCHNGG 542

QY 494 TCHQRQRYMCECAQGYGGPNCQFLLPEPPPPMVVDLSERHMESQG-----GPPFWAV 548
Db 543 TCMNRVNSFECVCANGFRGKQCD---EESYDSVTFDAHQYGATTQARADGLANAQVLI 598

QY 549 CAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGETETMNNLANCORE-KDVSVSII 607
Db 599 AVFSVAMPLVAVIAACVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALA 658

QY 608 GATQIKNTNKKADFHGDHG 626
Db 659 SASMGGKTGSNSGLTFDGG 677
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RESULT 8  
A56136  
jagged protein precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 21-Jul-2003  
C;Accession: A56136  
R;Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.  
Cell 80, 909-917, 1995  
A;Title: Jagged: a mammalian ligand that activates Notch1.  
A;Reference number: A56136; MUID:95211842; PMID:7697721  
A;Accession: A56136  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-1220 <LIN>  
A;Cross-references: GB:L38483  
F;379-410/Domain: EGF homology <EGF1>  
F;492-523/Domain: EGF homology <EGF>  
F;634-665/Domain: EGF homology <EGF2>

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Query Match      31.8%; Score 1312; DB 2; Length 1220;
Best Local Similarity 40.6%; Pred. No. 8.8e-74;
Matches 239; Conservative 78; Mismatches 215; Indels 56; Gaps 11;

QY 2 GRRSALALAVVSALLCQV-WSSGVFELKLQEFVNKKGLLGNRNCCR--GGSGPP--CA-- 54
Db 11 GRPLSLLALLCALRAKVCGASQGFELILSMQNVNVELQNGNCCAEPGTLVRPYKCTRD 70

QY 55 -CRTFFRVCLKHQASVSPEPPCTYGSVAVTPVLGVDSFSLPDGAGIDPAFSPNPIRFPFGF 113
Db 71 ECDTYFKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKASRGND---RNRIVLPFSF 127

QY 114 TWPGFSLIIEALHTDSPDDLATENPERLISRLLTQRHLTVGEWSQDLHSSGRTDLRYS 173
Db 128 AWPRSYTLLEA--WSSND--TIQPDSEIIEKASHSGMINPSROWOTLKONTGIAHFEYQ 183

QY 174 YRFVUDEHYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGYCTDPICLPGCDDQH 233
Db 184 IRVTCDDHYYGFGCNKFCRPRDDFFGHYACDQNGNKTCEGMWGPCECNKAICRQCSPKH 243

QY 234 GYCDKPGECKRVGWQGRYCDICIRYPCGVHGTCCQPWQCNCQBGWGLFCNQDLNYCTH 293
Db 244 GSCKLPGDCRCQYQWGLYCDKCIHPHPCGVHGTCTNEPWQCLCETNMGWQLCDKDLNYCGT 303

QY 294 HKPCRNAGATCTNTGQSYTCSRPGYTGANCEL----- 326
Db 304 HQPCLNRGTCSNTGPDKYQCSCPEGYSGPNCEIAEHACLSDPCHNRGSKETSSGFECEC 363

QY 327 -----EVDECAPSPCKNGASCTDLEDSFSCTCPPGYGKVCELSAMTCADGPFCF 375
Db 364 SPGWTGPTCSTNTIDDCSPNNCSHGTCQDLVNGFKVCVPPQWTGKTCQLDANECEAKPCV 423

QY 376 NGGRCSNPDGGYTCPLGFSGFENCEKKMDLCSSSPCSNGAKCVDLGNLYLCRCQAGFS 435
Db 424 NARSCK-NLIASYCDCLPGWMQNCNDINDC-LGQCQNDASCRDLVNGYRCICPPGYA 481

QY 436 GRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGATC 495
Db 482 GDHCERDIDECASNPCLNGGHQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQGAQC 541

QY 496 HQRGQRYMCECAQGYGGPNCQFLLPEPPPGPM-VVDLSERHMESQGGP 542
Db 542 YNRASDYFCPCPEDYEGKNCSHLKDHCRTPCEVIDSDCTVAMASNDTP 589
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RESULT 9  
S16148  
gene serrate protein precursor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 31-Dec-1991 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C;Accession: S16148; S16878; A36666  
R;Thomas, U.; Speicher, S.A.; Knust, E.  
Development 111, 749-761, 1991  
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co  
A;Reference number: S16148; MUID:91347903; PMID:1840519  
A;Accession: S16148  
A;Molecule type: mRNA  
A;Residues: 1-1408 <THO1>  
A;Cross-references: UNIPROT:P18168; EMBL:X56811  
R;Thomas, U.  
submitted to the EMBL Data Library, November 1990  
A;Reference number: S16878  
A;Accession: S16878  
A;Molecule type: mRNA  
A;Residues: 1-1351,'T',1353-1408 <THO2>  
A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564

R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2188-2201, 1990  
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential for  
A;Reference number: A36666; MUID:91099666; PMID:2125287  
A;Accession: A36666  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15,20-26,'A',28-1408 <FLE>  
A;Cross-references: GB:M35759; NID:g158605; PID:g158606  
C;Genetics:  
A;Gene: FlyBase:Ser  
A;Cross-references: FlyBase:FBgn0004197  
C;Keywords: glycoprotein; transmembrane protein  
F;1-84/Domain: signal sequence #status predicted <SIG>  
F;85-1408/Product: gene serrate protein #status predicted <MAT>  
F;85-1221/Domain: extracellular #status predicted <EXT>  
F;283-316/Domain: EGF homology <EG01>  
F;319-348/Domain: EGF homology <EG02>  
F;355-388/Domain: EGF homology <EG03>  
F;395-488/Domain: EGF homology #status atypical <EG04>  
F;495-526/Domain: EGF homology <EG05>  
F;533-608/Domain: EGF homology #status atypical <EG06>  
F;615-645/Domain: EGF homology <EG07>  
F;652-683/Domain: EGF homology <EG08>  
F;690-720/Domain: EGF homology <EG09>  
F;727-796/Domain: EGF homology #status atypical <EG10>  
F;803-834/Domain: EGF homology <EG11>  
F;841-876/Domain: EGF homology <EG12>  
F;883-914/Domain: EGF homology <EG13>  
F;921-952/Domain: EGF homology <EG14>  
F;997-1060/Region: cysteine-rich  
F;1222-1246/Domain: transmembrane #status predicted <TM1>  
F;1247-1408/Domain: intracellular #status predicted <INT>  
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn  
Query Match 27.4%; Score 1130; DB 2; Length 1408;  
Best Local Similarity 33.0%; Pred. No. 1.9e-62;  
Matches 226; Conservative 72; Mismatches 197; Indels 190; Gaps 16;  
Qy 7 LALAVVSALLCQVWSSGVFELKIQEFVNKGLLGNRNCCRGSGPP-----CA-C 55  
Db 69 LIALILLLVHKISAAGNFELEILEISNTNSHLLNGYCC---GMPAELRATKKTIGCSPC 124  
Qy 56 RTFFRVCLKHYQ-----ASVSPEPPCTYGSVTPVLGVDSFSLPD-GAGIDPAFSNPIRF 109  
Db 125 TTAFLRLCLKEYQTTEQASIS--TGCsFGNATTKILGSSsFVLSDPGVG-----AIVL 175  
Qy 110 PFGFTWPGTFSLIIEAL--HTDSPDDLATENPERLISRLTTQRLHTVGEWSQDLHSSG 166  
Db 176 PFTFRWTKSFTLILQALDMYNTSPD-----AERLIEETSYSGVILPSPWKTLDHGR 229  
Qy 167 RTDLRSYRFVCDHEYHGGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKQYCTDPICL 226  
Db 230 NARITYRVVQCAVYYNTTCTTFCRPRDDQFGHYACGSEQKLCNLNGWQGVNCEAICK 289  
Qy 227 PGDDOHGYCDKPGECKCRVGMQGRYCDECIRYPGCVHGTQ-QPWQCNCQEGWGLFCN 285  
Db 290 AGCDPVHGKCDRPGECECRPGWRGPLCNECMVYPGCKHSGCSAWKCVCDTNWGGILCD 349  
Qy 286 QDLNVCTHHKPCRNGATCTNTQGSY-----GDRGKMC-DPGWKQGYC-----TD 222  
Db 350 QDLNFCGTHEPKCHGGTCENTAPDKYRCTCAEGLSGEQCEIVEHPCATRPCRNGGTCTLK 409  
Qy 312 -----GDRGKMC-DPGWKQGYC-----TD 222  
Db 410 TSNRTQAQVYRTSHGRSNMGRVPRSSSMRSLDHLRPEGQALNGSSSGLVSLGLQIQ 469  
Qy 312 -----TCSCRPGYTGANCELEVDCAPSCKNGASCTDLEDSFSCTCPPGFYKVCBELS 365  
Db 470 QLAPDFTCDCAAGWTGPTCEINIDECAGGFCHEGGTCIDLIGGFRCECPPEWHGVDVCQVD 529  
Qy 366 AMTC-----ADGPCFNGGRCS 381

Db 530 VNECEAPHSAGIAANALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECR 589  
Qy 382 DNPDDGGYTCHCPLGFGFENCEKKMDLCSGSSPCSNAGAKCVDLGNSYLCRCQAGFSGRYCED 441  
Db 590 NQP-GSFACICKEGWGGVTCAENLDDC-VGQCRNGATCIDLVNDYRCACASGFTGRDCET 647  
Qy 442 NVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCsAPVSRCEHAPCHNGATCHQRGQR 501  
Db 648 DIDECATSPCRNGGECVDMVGKFNICICPLGYSGLCEBAKENCTPSPCLEG-HCLNTPEG 706  
Qy 502 YMCECAQGYGGPNCQFLLP---EPP 523  
Db 707 YYCHCPPDRAGKHCEQLRPLCSQPP 731  
RESULT 10  
A35844  
Xotch protein - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 16-Aug-2004  
C;Accession: A35844  
R;Coffman, C.; Harris, W.; Kintner, C.  
Science 249, 1438-1441, 1990  
A;Title: Xotch, the Xenopus homolog of Drosophila notch.  
A;Reference number: A35844; MUID:90385285; PMID:2402639  
A;Accession: A35844  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: mRNA  
A;Residues: 1-2524 <COF>  
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: transmembrane protein  
F;146-177/Domain: EGF homology <EGX1>  
F;184-215/Domain: EGF homology <EGF1>  
F;222-254/Domain: EGF homology <EGF>  
F;456-487/Domain: EGF homology <EGX2>  
F;757-788/Domain: EGF homology <EGF3>  
F;1025-1056/Domain: EGF homology <EGX3>  
F;1924-1956/Domain: ankyrin repeat homology <AN1>  
F;1957-1989/Domain: ankyrin repeat homology <AN2>  
F;1991-2023/Domain: ankyrin repeat homology <AN3>  
F;2024-2056/Domain: ankyrin repeat homology <AN4>  
F;2057-2089/Domain: ankyrin repeat homology <AN5>  
Query Match 19.7%; Score 810; DB 2; Length 2524;  
Best Local Similarity 31.6%; Pred. No. 2.1e-42;  
Matches 184; Conservative 61; Mismatches 196; Indels 142; Gaps 21;  
Qy 44 CCRGSGPPCACRTFFRVCLKHYQASVS--PEPCTYGSVTPVLGVDSFSLPDGAGID 100  
Db 543 CLDGPNSYTCQCTEGFTG--RHCEQDINECIPD-PCHYGTG-----KDGIA TF 587  
Qy 101 PAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRLHTV----- 155  
Db 588 TCLCRP-----GYTGRLCDNDINECL--SKPCLNGGQCTDRENGYICTCPKGTGVNCET 640  
Qy 156 --BEWSQDLHSSGR-TDLRSYRFVCDHEYHGGCSVFCRPRD-----DAFGHF 201  
Db 641 KIDDCASNLCNDNGKCIDKIDGYECTCEPGYTGKLCNININECDsNPCRNGGTCKDQINGF 700  
Qy 202 TC-----GDRGKMC-DPGWKQGYC-----TD 222  
Db 701 TCVCPDGYHDMCLSEVNECNSNPICIHGACHDGVNGYKCDCEAGWSGNSCDINNNECESN 760  
Qy 223 PICLPG--CDDQHG-YCDKPGECKCRVGMQGRYC----DECIRYPGCVHGTG----- 267  
Db 761 P-CWNGGTCKDMTGAYI-----CTKAGFSGPNQCNTNINECSSNPCLNHGTCTIDDVAGYK 814  
Qy 268 -----QQPWQCNCQEGWGLFCNQDLNYCT 292  
Db 815 CNCMLPYTGAICEAVLAPCAGSPCKNGGRCKESEDFFETSCCEPPGWQGTCEIDMNECV 874  
Qy 293 HHKPCRNGATCTNTQGSYTCSRPGYTGANCELEVDCAPSCKNGASCTDLEDSFSCT 352

Db 875 -NRPCRNATCQNT-NGSYKCNCKPGYTGRNCEMIDDDCQPNPCHNGGSCSDGINMFFCN 932

Qy 353 CPPGFYKVCELSAMTCADGPCFNGGRCSNDPDGGYTCHCPLGFSGFNCEKXMDLGGSSP 412

Db 933 CPAGFRGPKCEEDINECASNPCKNGANCCTDCVN-SYTCTCQPGFSGIHCSNTPDCTESS 991

Qy 413 CSNGAKCVDLGNLYLRCQAGFSGRYCEVDNDCASSPCANGGTCRDSVNDPSCCTCPPGY 472

Db 992 CFNGGTCTIDGINTFTCQCPGFTGSYCQHDINECDKPCNLGGTCQDSYGTYKCTCPQGY 1051

Qy 473 TGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNC 515

Db 1052 TGLNCQNLVVRWCDSPPCKNGGKCQWQTNFYRCECKSGWTGVYC 1094

RESULT 11

A46019

notch-1 protein - mouse

N;Alternate names: notch protein

C;Species: Mus musculus (house mouse)

C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004

C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109

R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid

Genomics 15, 259-264, 1993

A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of

A;Reference number: A46019; MUID:93194170; PMID:8449489

A;Accession: A46019

A;Status: not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-2531 <DEL>

A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:G288502; PIDN:CAA77941.1;

A;Note: sequence extracted from NCBI backbone (NCBIP:127318)

R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;

submitted to the EMBL Data Library, April 1992

A;Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest

A;Reference number: S25144

A;Accession: S25144

A;Molecule type: mRNA

A;Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>

A;Cross-references: EMBL:Z11886

R;Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety o

A;Reference number: A49175; MUID:93178563; PMID:8440332

A;Accession: C49175

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1161-1547 <LAR>

A;Cross-references: EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PID:G287988

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIP:126159)

R;Kopan, R.; Weintraub, H.

J. Cell Biol. 121, 631-641, 1993

A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati

A;Reference number: A46438; MUID:93252998; PMID:8486742

A;Accession: B46438

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)

C;Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.

C;Genetics: This protein is one of the neurogenic proteins controlling the decision betwe

A;Gene: notch-1

A;Map position: 2

A;Note: proximal region of chromosome 2

C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F;106-138/Domain: EGF homology <EGF1>

F;144-175/Domain: EGF homology <EG01>

F;222-254/Domain: EGF homology <EGF2>

F;261-292/Domain: EGF homology <EG02>

F;339-370/Domain: EGF homology <EG03>

F;416-449/Domain: EGF homology <EGF3>

F;456-487/Domain: EGF homology <EG04>

F;494-525/Domain: EGF homology <EG05>

F;532-563/Domain: EGF homology <EG06>

F;607-638/Domain: EGF homology <EG07>

F;682-713/Domain: EGF homology <EG08>

F;757-788/Domain: EGF homology <EG09>

F;795-826/Domain: EGF homology <EG10>

F;873-904/Domain: EGF homology <EG11>

F;911-942/Domain: EGF homology <EG12>

F;949-980/Domain: EGF homology <EG13>

F;987-1018/Domain: EGF homology <EG14>

F;1025-1056/Domain: EGF homology <EG15>

F;1063-1094/Domain: EGF homology <EG16>

F;1149-1180/Domain: EGF homology <EG17>

F;1187-1218/Domain: EGF homology <EG18>

F;1233-1264/Domain: EGF homology <EGF4>

F;1352-1383/Domain: EGF homology <EG19>

F;1391-1425/Domain: EGF homology <EGF>

F;1917-1948/Domain: ankyrin repeat homology <AN1>

F;1949-1981/Domain: ankyrin repeat homology <AN2>

F;1983-2015/Domain: ankyrin repeat homology <AN3>

F;2016-2048/Domain: ankyrin repeat homology <AN4>

F;2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 19.6%; Score 807.5; DB 2; Length 2531;

Best Local Similarity 28.3%; Pred. No. 3e-42;

Matches 223; Conservative 60; Mismatches 252; Indels 253; Gaps 31;

Qy 45 CRGGS-----GPPCACRTFFRVCLKHQAS-----VSPEPPCTYGSATVPVLGVDSFS 92

Db 537 CKNGAKCLDGP---NTYTCVCTEGYTGTHCEVDIDECDPD-PCHYGSCKDGVATFTCLC 591

Qy 93 LPDGAG-----IDPAFSNPIRFPFGFTWPGTFS-----LIIEALHTDSP-----DDL 134

Db 592 QPGYTGHHCHETNINECHSQPCRH-----GGTCQDRDNSYLCCLKGTGPNCEINLDDC 645

Qy 135 ATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCEHYHGECSV----- 189

Db 646 AS-NP-----CDSGTCLDKIDGYECACEPGYTGSMCNVNIDEC 682

Qy 190 -----FCRPRDDAFGHFTC-----GDRGEKM 210

Db 683 AGSPCHNGGTC---EDGIAGFTCRCPGEGYHPTCLSEVNECNSNPCIHGACRDGLNGYKC 739

Qy 211 -CDPGWKQGYC-----TDPICLPG--CDDQ-HGYCDKPGCECKRVGWQGRYC-----D 254

Db 740 DCAPGWSGTNCDINNNECESNP-CVNGGTCCKDMTSGYV-----CTCREGFSGPNCQTNIN 793

Qy 255 ECIRYPGCVHGTC-----QQPW 271

Db 794 ECASNPCNLNGGTCIDDVAGYKCNCPLPYTGATCEVVLAPCATSPCKNSGVCKESEDYESF 853

Qy 272 QCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTQGSGYTCSCRPGYTGANCELEVDEC 331

Db 854 SCVCPTGWQGTCEVDINECV-KSPCRHGASCQNT-NGSYRCLCQAGYTGRCNESDIDDC 911

Qy 332 APSCKNGASCTDLEDSEFSCTCPPGFYGVKVCELSAMTCADGCPCFNGGRCSDNPDGGYTCH 391

Db 912 RPNPCHNGSGCTDGINAFCDCLPGFGAFCEEDINECASNPQNGANCCTDCVD-SYTCT 970

Qy 392 CPLGFSGFNCEKKMDLCGSSPCSNAGKACVDLGNLYLRCQAGFSGRYCEVDNDDCASSPC 451

Db 971 CPVGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPGFTGSYCQYDVNECDSRPC 1030

Qy 452 ANGGTCRDSVNDPSCCTCPPGYTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYG 511

Db 1031 LHGGTCQDSYGYTKCTCPQGYTGLNCQNLVRWCDSAPCKNGGRCWQNTNTQYHCECRSGWT 1090

Qy 512 GPNQCQFLLPE-----PPPGPMVVDLSERHMESQGGFPFWAVACAGVVLVL 556

Db 1091 GVNCDVLSVCEVAAQKRIGIDVTLLCQHGLCVDEGDKH----- 1129



QY 557 LLLGCAAVVVCVRLKLQKHQPPPCGGETETMTNNLANCQREKDVSVSIIGATQIKNTN 616  
Db 1130 --YCHCQAGYTGSCYCEDEVDECSNPNC-----QNGATC-----TDYLGGFSCKCV- 1172  
QY 617 KKADFHGDHGAEKSSFVKVRYPTVDYNLVRDLKGD-----EATVRDTH---- 658  
Db 1173 --AGYHGSNCSEEEINECLSQPCQNGGTCIDLNTNSYKSCSPRGQTQGVHCEINVDCHPPLD 1230  
QY 659 -SKRDTKC 665  
Db 1231 PASRSPKC 1238  
RESULT 12  
S18188  
notch protein homolog - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C;Accession: S18188  
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.  
Development 113, 199-205, 1991  
A;Title: A homolog of Drosophila Notch expressed during mammalian development.  
A;Reference number: S18188; MUID:92111383; PMID:1764995  
A;Accession: S18188  
A;Molecule type: mRNA  
A;Residues: 1-2531 <WEI>  
A;Cross-references: EMBL:X57405; NID:957634; PID:957635  
C;Superfamily: notch protein; ankyrin repeat homolog; EGF homolog  
F;987-1018/Domain: EGF homolog <EGF1>  
F;1025-1056/Domain: EGF homolog <EGF>  
F;1233-1264/Domain: EGF homolog <EGF2>  
F;1917-1949/Domain: ankyrin repeat homolog <AN1>  
F;1950-1982/Domain: ankyrin repeat homolog <AN2>  
F;1984-2016/Domain: ankyrin repeat homolog <AN3>  
F;2017-2049/Domain: ankyrin repeat homolog <AN4>  
F;2050-2082/Domain: ankyrin repeat homolog <AN5>  
Query Match 19.3%; Score 794.5; DB 2; Length 2531;  
Best Local Similarity 27.9%; Pred. No. 1.9e-41;  
Matches 226; Conservative 64; Mismatches 268; Indels 253; Gaps 32;  
QY 28 KLOEFVNK--KGLLGN-----RNC-----CRGGS-----GPPCACRTFFRVCLKHQYQAS-- 69  
Db 508 KINEFLCQCPKFGFSGHLCCQYDVDECASTPCKNGAKCLDGP---NTYTCVCTEGYGTGTHC 563  
QY 70 -----VSPEPPCTYGSAVTPVLGVDSFSLPDGAG-----IDPAFSNPPIRFPFGFTWPG 117  
Db 564 EVDIDECDPD-PCHIGLCKDGVATFTCLCPQGYTGHHCEITNINECHSQPCRHHGFTCQDRD 622  
QY 118 TFSLIIEALHTDSP-----DDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLR 171  
Db 623 NYVLCCLCLKGTTGPNCEINLDDCAS-NP-----CDSGTCLDKI 659  
QY 172 YSYRFVCDHEYHGGCSV-----FCRPRDDAFGHFTC----- 203  
Db 660 DGYECACEPGYTGSMCNVNIDECAGSPCHNGGTC---EDGIAGFTCRCPEGYHDP TCLSE 716  
QY 204 -----GDRGSKM-CDPGWKQGYC-----TDPICLPG--CDDQ-HGY 235  
Db 717 VNECNSNPCTIHGACRDGLNGYKCDCAPGWSGTNCDINNNECESNP-CVNGGTCKDMTSGY 775  
QY 236 CDKPGECKRVGWQGRYC----DECIRYPGCVHGTC----- 267  
Db 776 V-----CTCREGFGSPNCQTNINECASNPCLNQGTCTDDVAGYKNCPLPYTGATCEVWL 830  
QY 268 -----QQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNGATCTNTGQ 308  
Db 831 APCATSPCKNSGVCKESEDYESFSCVPTGWQGTCEIDINECV-KSPCRHGASCQNT-N 888  
QY 309 GSYTCSCRPGYTGANCELEVDDECAPSPCKNGASCCTDLEDSFSCCTPPGFYGVKVCELSAMT 368  
Db 889 GSYRCLCQAGYTGRNCESDIDCRPNFCHNGGSCTDGVNAAFCDCLPFGQGFCEEDINE 948

QY 369 CADGPCFNGGRCSNDPDGGYTCHCPLGFSGFNCEKMKMDLCGSSPSCNGAKCVDLGNSYLC 428  
Db 949 CATNPCQNGANCTDCVD-SYTCTCPTGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTC 1007  
QY 429 RCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDPFSCTCPPGYTGKNCSAPVSRCEHAP 488  
Db 1008 LCPPGFTGSYCOYVNECDSRPCLHGGTCQDSYGYKCTCPQGYTGLNQNLVRWCDSAP 1067  
QY 489 CHNGATCHQQRQRYMCECAQGYGGPNCQFLLPE-----PPPQPMVVVDLSE 533  
Db 1068 CKNGGKCWQTNTQYHCECRSGWTGFNCVDVLSVSEVAAQKRIGIDVTLLCQHGGCLCDEED 1127  
QY 534 RHMESQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPCGGETETMNNL 593  
Db 1128 KH-----YCHCQAGYTGSCYCEDEVDECSNPNC-----QNG 1157  
QY 594 ANCQREKDVSVSIIGATQIKNTNKKADFHDHGAEKSSFKVRYPTVDYNLVRDLKGD--- 650  
Db 1158 ATC-----TDYLGGFSCKCV---AGYHGSNCSEBINECLSQPCQNGGTCIDLNTNYKC 1207  
QY 651 -----EATVRDTH-----SKRDTKC 665  
Db 1208 SCPRGTOGVHCEINVDCHPPLDPASRSPPKC 1238  
RESULT 13  
A40136  
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)  
N;Alternate names: epidermal growth factor homolog precursor  
N;Contains: alternatively spliced fibropellin Ib (EGFI)  
C;Species: Strongylocentrotus purpuratus (purple urchin)  
C;Date: 13-May-1992 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: A40136; B40136; C40136; A29316; A43131  
R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.  
J. Mol. Evol. 29, 314-327, 1989  
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpur  
A;Reference number: A40136; MUID:90112459; PMID:2514273  
A;Accession: A40136  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <DEL>  
A;Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061  
A;Accession: B40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>  
A;Accession: C40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 'K',747-821,898-978 <DE3>  
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.  
Science 237, 1487-1490, 1987  
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.  
A;Reference number: A29316; MUID:87319677; PMID:3498216  
A;Accession: A29316  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 'S',280-481,786-1064 <HUR>  
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260  
R;Hunt, L.T.; Barker, W.C.  
FASEB J. 3, 1760-1764, 1989  
A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.  
A;Reference number: A43131; MUID:89196806; PMID:2784773  
A;Contents: annotation  
C;Comment: EGF homolog repeats 10-17 are spliced out in the short form (fibropellin Ib).  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-1064/Product: fibropellin I #status predicted <FIB>  
F;23-54/Domain: EGF homolog <EG01>  
F;57-175/Domain: C1r/C1s repeat homolog <C1R>  
F;180-211/Domain: EGF homolog <EG02>  
F;218-249/Domain: EGF homolog <EG03>  
F;256-287/Domain: EGF homolog <EG04>  
F;294-325/Domain: EGF homolog <EG05>



F;332-363/Domain: EGF homology <EG06>  
F;370-401/Domain: EGF homology <EG07>  
F;408-439/Domain: EGF homology <EG08>  
F;446-477/Domain: EGF homology <EG09>  
F;484-515/Domain: EGF homology <EG10>  
F;522-553/Domain: EGF homology <EG11>  
F;560-591/Domain: EGF homology <EG12>  
F;598-629/Domain: EGF homology <EG13>  
F;636-667/Domain: EGF homology <EG14>  
F;674-705/Domain: EGF homology <EG15>  
F;712-743/Domain: EGF homology <EG16>  
F;750-781/Domain: EGF homology <EG17>  
F;788-819/Domain: EGF homology <EG18>  
F;826-857/Domain: EGF homology <EG19>  
F;864-895/Domain: EGF homology <EG20>  
F;902-933/Domain: EGF homology <EG21>  
F;936-1064/Region: avidin-like  
F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27  
57,451-466,468-477,484-495/Disulfide bonds: #status predicted  
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62  
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disul

Query Match 18.7%; Score 771; DB 2; Length 1064;  
Best Local Similarity 31.8%; Pred. No. 2.5e-40;  
Matches 174; Conservative 45; Mismatches 188; Indels 140; Gaps 17;

QY 177 VCDEHYYGEGCSV-----FCRPRDDAFGHFTCGDRGE-----KMCDPGWKGQYC 220  
Db 304 ICIDGINGYTCSPFGSGDNCENNDECSSIPCLNGGTCVDLVNAYMVCAPGWTGPTC 363  
QY 221 TDPI-----CLPG-----CDDQHGY-----CDKPGECK--- 243  
Db 364 ADNIDECASAPCQNGVCIDGVNGYMCDCQPGYTGTHCETDIDECARPPCQNGGDCVDGV 423  
QY 244 -----CRVGWQGRYC-----DECIRYP-----CCVHGTCQQPWQCNCQEGWGLFCNQDL 288  
Db 424 NGYVCICAPGFDGLNCENNIDECASRPCQNGAVCVDGV--NGFVCTCSAGYTGVL CETDI 481  
QY 289 NYCTHHKPCRNGATCTNTGQGSYTCSCRPRGYTGANCELEVEDECAPSPCKNGASC TDLEDS 348  
Db 482 NECA-SMPCNLNGGVCTDLVNG-YICTCAAGFEGTNCETDTDECASFPCQNGATCTDQVNG 539  
QY 349 FSCTCPPGFYKVCELSAMTCADGPCFNGGRCSDNPDG----- 386  
Db 540 YVCTCVPGYTGVL CETDINECASFPCLNGGTCNDQWNGYVCVCAQDTSVSTCETDRDECA 599  
QY 387 -----GYTCHCPLGFGFNCBKKMDLCGSSPCSNGA KCVDLGN SYLCRCQ 431  
Db 600 SAPCLNGGACMDVNGFVCTCLPGWEGTNCINTDECASSPCMNGLCV DQVNSYVCFCL 659  
QY 432 AGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHN 491  
Db 660 PGFTGIHCGTETDECASSPCLNGGQCIDRVDSYECVCAAGYTA VRCQINIDECASAPCQN 719  
QY 492 GATCHQRGQRYMCECAQGYGGPNQCQFLPPEPPGPMVV DLSERHMESQGGFPFWAVCAG 551  
Db 720 GGVCVDGVNGYVCNCAPGYTGDNCE TEIDECASMPCL-----NGG-----AC 761  
QY 552 VVLVLLLLLGC AA VVVCVRLKLQKHQPPPEPC--GGE-TETMNNL-----ANCQR 598  
Db 762 IEMVNGYTCQC VAGYTGVICETDIDECASAPCQNGGVCTDTINGYICACVPGFTG S NCET 821  
QY 599 EKDVSVS 605  
Db 822 NIDECAS 828

RESULT 14  
S42612  
transmembrane protein precursor - zebra fish  
C;Species: Brachydanio rerio (zebra fish)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S42612

R;Bierkamp, C.; Campos-Ortega, J.A.  
Mech. Dev. 43, 87-100, 1993  
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern o  
A;Reference number: S42612; MUID:94128602; PMID:8297791  
A;Accession: S42612  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2437 <BIE>  
A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:G433866; PIDN:CAA4831.1; PID:G4338  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F;755-786/Domain: EGF homology <EGF1>  
F;1023-1054/Domain: EGF homology <EGF>  
F;1185-1216/Domain: EGF homology <EGF2>  
F;1915-1947/Domain: ankyrin repeat homology <AN1>  
F;1948-1980/Domain: ankyrin repeat homology <AN2>  
F;1982-2014/Domain: ankyrin repeat homology <AN3>  
F;2015-2047/Domain: ankyrin repeat homology <AN4>  
F;2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 18.6%; Score 765.5; DB 2; Length 2437;  
Best Local Similarity 32.9%; Pred. No. 1.2e-39;  
Matches 168; Conservative 57; Mismatches 203; Indels 82; Gaps 19;

QY 44 CCRGGSGPPCA-----CRTFFRVLKHYQASVSPPEPCTYGS AVTPVLGVDSFSLPDGAG 98  
Db 627 CPKGTGVNCEINIDCK-----RKPCDYGKCIDKINGIECVCEPGYSG 670  
QY 99 -----IDPAFSNPIRPFPGFTWPGFSLIIEALHTDSPDDLATENPERLISRLTTQRHL 152  
Db 671 SMCNINIDCALNPCHN-----GGTC-----IDGVNSFTCLCPDGRDATCLSQH- 715  
QY 153 TVGEWSQD--LHSSGRTDLRYSYRFVCDHEHYGEGCSV---FCRPRDDAFGHFTCGDRG 207  
Db 716 ---NECSSNPCIHGSCLDQIN-SYRCVCBAGWMGRNC DININECLSNPCVNGG-TCKDMT 770  
QY 208 EK---MCDPGWKGYC-----TDPICLPG--CDDQHGYCDKPGECKCRVWQGRYCD 254  
Db 771 SGYLCTCRAGFSGPNCQM NINECASNPCLNQSGCIDDVAGF-----KNCNMLPYTGEVCE 825  
QY 255 E----CIRYPCGVHGTQ-----QPWQCNCQEGWGLFCNQDLNYCTHHKPCRNGATCTN 305  
Db 826 NVLAPCSRPCKNGGVCRESEDFQSFSCNPAGWQGTCEVDINECVRN-PCTNGGV CEN 884  
QY 306 TQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASC TDLEDSFSCTCPPGFYKVCELS 365  
Db 885 L-RGGFQRCRNPFGFTGALCENDIDDCENPCSNGGVCQDRVNGFVCVCLAGFRGERCAED 943  
QY 366 AMTCADGPCFNGGRCSNDPDGGYTHCPLGFGFNCBKKMDLCGSSPCSNGA KCVDLGN S 425  
Db 944 IDECVSAPCRNGGNC TDCVN-SYTCSPAGFSGINCEINTPDCTESSCFNGGTCVDGISS 1002  
QY 426 YLCRCQAGSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCE 485  
Db 1003 FSCVCLPGFTGNYCQHDVNECDSRPCQNGSGCQDGYGTYKCTCPHGYTGLNCQSLVRWCD 1062  
QY 486 HAPCHNGATCHQRQRYMCECAQGYGGPNC 515  
Db 1063 SSPCKNGSGSCWQQQASFTCCQCASGWTGIYC 1092

RESULT 15  
A49175  
Motch B protein - mouse (fragment)  
N;Alternate names: Notch homolog  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Jan-1994 #sequence\_revision 05-Jan-1996 #text\_change 16-Aug-2004  
C;Accession: A49175; PH1570; S32113  
R;Lardelli, M.; Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety o  
A;Reference number: A49175; MUID:93178563; PMID:8440332  
A;Accession: A49175  
A;Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-1203 <LAR>  
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287989  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)  
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.  
C:Comment: This protein is one of the neurogenic proteins controlling the decision between  
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
F:143-174/Domain: EGF homology <EGX1>  
F:482-513/Domain: EGF homology <EGF1>  
F:560-591/Domain: EGF homology <EGF>  
F:674-705/Domain: EGF homology <EGX2>  
F:712-743/Domain: EGF homology <EGF3>  
F:836-867/Domain: EGF homology <EGX3>

Query Match	18.5%;	Score 761;	DB 2;	Length 1203;
Best Local Similarity	32.2%;	Pred. No. 1.2e-39;		
Matches 186;	Conservative 61;	Mismatches 216;	Indels 114;	Gaps 21;

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QY      39  LGNRNCRGGSGPPCACRTFFRVCLKHVQASVSEPPCTYGSVAVTPVLGVDSFSLPDGAG 98
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Db      225  LNGAKCIDHPNGYECQCATGFTGILCDENIDNCDPDPCHHGQCQD---GIDSYTCICNPG 281
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY      99  -----IDPAFSNP-----IRFPFGF---TWPGTFLIIIEALHTDSPDDLATENP 139
           ||  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      282  YMGAIQSDQIDECYSSPCLNDGRCLDLVNGYQCNCQPGTSLNCEI---NFDDCAS-NP 336
           ||  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

QY     140  -----ERLISR-----LTTQRHLTVGEBSQDLHSSGRTDLR--YSYRFVCDEHY 183
           ||  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db     337  CMHGVCVGGINRYSCVSPGFTGQRCNIDIDECASNPCRKGATCINDVNGFRICPEGPH 396
           ||  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

QY     184  GEGCSV---FCRPRDDAFGHFTCGDRGEK-MCDPGWKQGYC-----TDPICLPG--C 229
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     397  HPSCYSQVNECLSNPNCIHNCTGGLSGYKCLDAGWVGWVNCVVDKNECLSNP-CQNGGTC 455
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY     230  DD-QHGYCDKPGCKCRVWGQRYC-----DECIRYPGCVHGT----- 267
           ::  :  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     456  NNLVNGY-----RCTCKKGFGYNCQVNIDECASNPCNLNQGTCTFDDVSGYTCHCMLPYTG 510
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY     268  -----QQPWQNCQEGWGGLFCNQDLNLYCTHHKPCRNGA 301
           :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     511  KNCQTVLAPCSNPENCAAVCKEAPNFESFSLCAPGWQGRKCTVDVDECI-SKPCMNG 569
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY     302  TCTNTGQGSYTCSCRPPGYTGANCELEVDCAFPSPCKNGASCCTDLEDSEFSCCTPPGPGVKV 361
           ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db     570  VCHNT-QGSYVCECPPGFGMDCEEDINDCLANPCQNGGSCVDHVNTFSCQCHPGFIGDK 628
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY     362  CELSAMTCADGPCFNGGRCSDNPDGGYTCHCPGLGFSGFNCEKKMDLCGSSPCSNGAKCVD 421
           |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     629  CQTDMECLSEPCKNGGTCSDYVN-SYTCTCPAGFHGVHCENNIDECTESSCFNGGTCTVD 687
           ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

QY     422  LGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSDVNDFSCTCPPGYTGKNCSAPV 481
           ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db     688  GINSFSLCPVGTGTPFCLHDINECSSNPCLNAGTCVDGLGYRCICPLGYTGKNCQTLV 747
           ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

QY     482  SRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQCFL 518
           :  :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     748  NLCSSRSPCKNKGTCVQEKARPHCLCPPGWGDGAYCDVL 784
           :  :  |  |  |  |  |  |  |  |  |  |  |  |

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 86.9238 Seconds  
(without alignments)  
4779.132 Million cell updates/sec

Title: US-09-783-931-12  
Perfect score: 4121  
Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4007	97.2	722	2	Q6PFV7
2	4007	97.2	722	2	AAH57400
3	4007	97.2	722	2	AAR30869
4	4007	97.2	722	2	AAH65063
5	4003	97.1	722	1	DL11_MOUSE
6	3848	93.4	713	1	DL11_RAT
7	3652.5	88.6	723	1	DL11_HUMAN
8	3368	81.7	728	2	Q90656
9	3167.5	76.9	721	2	Q91902
10	3146	76.3	726	2	Q8AW87
11	2826.5	68.6	720	2	Q8UWJ4
12	2823.5	68.5	717	2	P87357
13	2778	67.4	772	2	Q6DI48
14	2713	65.8	802	2	O57462
15	1902	46.2	642	2	Q7ZXT4
16	1896	46.0	642	2	P79941
17	1879.5	45.6	685	1	DL14_HUMAN
18	1832	44.5	686	1	DL14_MOUSE
19	1828	44.4	686	2	Q9DBU9
20	1810.5	43.9	664	2	Q91AT6
21	1775.5	43.1	615	2	O57409
22	1630.5	39.6	684	2	Q8I498
23	1472	35.7	650	2	Q7Q0M5
24	1469.5	35.7	833	2	Q6T4M9
25	1469.5	35.7	833	2	Q6T4N0
26	1469.5	35.7	833	2	Q6T4N1
27	1469.5	35.7	833	2	Q6T4N2
28	1469.5	35.7	833	2	Q6T4N6
29	1469.5	35.7	833	2	AAR21453
30	1469.5	35.7	833	2	AAR21454
31	1469.5	35.7	833	2	AAR21461

32	1469.5	35.7	833	2	AAR21462	Aar21462 drosophil
33	1469.5	35.7	833	2	AAR21463	Aar21463 drosophil
34	1469.5	35.7	833	2	AAR21464	Aar21464 drosophil
35	1468.5	35.6	833	1	DL DROME	P10041 drosophila
36	1468.5	35.6	833	2	Q6T4N3	Q6t4n3 drosophila
37	1468.5	35.6	833	2	Q6T4N4	Q6t4n4 drosophila
38	1468.5	35.6	833	2	AAO25024	Aao25024 drosophil
39	1468.5	35.6	833	2	AAR21455	Aar21455 drosophil
40	1468.5	35.6	833	2	AAR21456	Aar21456 drosophil
41	1468.5	35.6	833	2	AAR21457	Aar21457 drosophil
42	1468.5	35.6	833	2	AAR21458	Aar21458 drosophil
43	1468.5	35.6	833	2	AAR21459	Aar21459 drosophil
44	1468.5	35.6	833	2	AAR21460	Aar21460 drosophil
45	1468.5	35.6	833	2	AAR21465	Aar21465 drosophil

ALIGNMENTS

RESULT 1  
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ID Q6PFV7 PRELIMINARY; PRT; 722 AA.  
AC Q6PFV7;  
DT 05-JUL-2004 (TremBLrel. 27, Created)  
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
DT 01-OCT-2004 (TremBLrel. 28, Last annotation update)  
DE Delta-like 1.  
GN Name=Dll1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RN [4]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Nagajara R., Waeltz P., Brathwaite M.E.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;  
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 8 EGF-like domains.  
DR EMBL; BC057400; AAH57400.1; -.  
DR EMBL; BC065063; AAH65063.1; -.  
DR EMBL; AY497019; AAR30869.1; -.  
DR GO; GO:000515; F:protein binding; IPI.  
DR GO; GO:0007386; P:compartment specification; IMP.  
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.  
DR GO; GO:0001757; P:somite specification; IMP.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR Pfam; PF07645; EGF\_CA; 1.  
DR PRINTS; PR00010; EGFBLLOOD.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00181; EGF; 8.  
DR SMART; SM00179; EGF\_CA; 6.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW EGF-like domain.  
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;  
  
Query Match 97.2%; Score 4007; DB 2; Length 722;  
Best Local Similarity 97.4%; Pred. No. 4.6e-269;  
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;  
  
Qy 1 MGRSALALAVVSALLCQVWSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60  
Db 1 MGRSALALAVVSALLCQVWSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60  
  
Qy 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120  
Db 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120  
  
Qy 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180  
  
Qy 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240  
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240  
  
Qy 241 ECKCRVWQGRYCDICIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
Db 241 ECKCRVWQGRYCDICIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
  
Qy 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPPGFYGK 360  
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPPGFYGK 360  
  
Qy 361 VCLSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFGSGNCEKMDLCGSSPCSNCAKCV 420  
Db 361 VCLSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFGSGNCEKMDLCGSSPCSNCAKCV 420  
  
Qy 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDRSVNDFSCTCPPGYTKNCSAP 480  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCDRSVNDFSCTCPPGYTKNCSAP 480  
  
Qy 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNQCQLLPEPPPGPMVVDLSERHMSQG 540  
Db 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNQCQLLPEPPPGPMVVDLSERHMSQG 540

Qy 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPEPCGGTETMNNLANCQREK 600  
Db 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHOPPEPCGGTETMNNLANCQREK 600  
  
Qy 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
Db 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
  
Qy 661 RDTKCQSOSLQEKRRSPQHILGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720  
Db 661 RDTKCQSOSAGEEKIAPTILRGGEIPDKRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720  
  
Qy 721 EV 722  
Db 721 EV 722  
  
RESULT 2  
AAH57400  
ID AAH57400 PRELIMINARY; PRT; 722 AA.  
AC AAH57400;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Delta-like 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057400; AAH57400.1; -.  
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 97.2%; Score 4007; DB 2; Length 722;  
Best Local Similarity 97.4%; Pred. No. 4.6e-269;  
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGRSALALAVVSALLCQVWSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60  
Db 1 MGRSALALAVVSALLCQVWSSGVFELKQLQEFVNKKGLGNRNCCRGSGPPCACRTFFR 60  
  
Qy 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120  
Db 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120



QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLLTVGEEWSQDLHSSGRTDLRYSRFFVCDE 180  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLLTVGEEWSQDLHSSGRTDLRYSRFFVCDE 180  
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCDDQHGKPCG 240  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCDDQHGKPCG 240  
QY 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
DB 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPGFYK 360  
DB 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPGFYK 360  
QY 361 VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKCV 420  
DB 361 VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKCV 420  
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
DB 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
QY 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540  
DB 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540  
QY 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600  
DB 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600  
QY 601 DVSVSIIGATQIKNTNKKADFHDGHAEEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
DB 601 DVSVSIIGATQIKNTNKKADFHDGHAEEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
QY 661 RDTKCQSQSAGEEKIAPTTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
DB 661 RDTKCQSQSAGEEKIAPTTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
QY 721 EV 722  
DB 721 EV 722

RESULT 3

AAR30869 PRELIMINARY; PRT; 722 AA.  
ID AAR30869  
AC AAR30869;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Delta like-1.  
GN DLL1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Nagaraja R., Waeltz P., Brathwaite M.E.;  
RT "Genomic Sequence Analysis in the Mouse t-complex Region."  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY497019; AAR30869.1; --  
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match

97.2%; Score 4007; DB 2; Length 722;

Best Local Similarity 97.4%; Pred. No. 4.6e-269;  
Matches 703; Conservative 3; Mismatches 16; Indels 0; Gaps 0;  
QY 1 MGRRSALALAVVSALLCQWSSGVFELKLQEFVKNKGLLGNRNCRCGGSGPPCARTFFR 60  
DB 1 MGRRSALALAVVSALLCQWSSGVFELKLQEFVKNKGLLGNRNCRCGGSGPPCARTFFR 60  
QY 61 VCLKHYQASVSPPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120  
DB 61 VCLKHYQASVSPPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPPIRFPFGFTWPGTFS 120  
QY 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLLTVGEEWSQDLHSSGRTDLRYSRFFVCDE 180  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLLTVGEEWSQDLHSSGRTDLRYSRFFVCDE 180  
QY 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCDDQHGKPCG 240  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKQYCTDPICLPGCDDQHGKPCG 240  
QY 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
DB 241 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
QY 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPGFYK 360  
DB 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPGFYK 360  
QY 361 VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKCV 420  
DB 361 VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNGAKCV 420  
QY 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
DB 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
QY 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540  
DB 481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540  
QY 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600  
DB 541 GPFPPWAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600  
QY 601 DVSVSIIGATQIKNTNKKADFHDGHAEEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
DB 601 DVSVSIIGATQIKNTNKKADFHDGHAEEKSSFVKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
QY 661 RDTKCQSQSAGEEKIAPTTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
DB 661 RDTKCQSQSAGEEKIAPTTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
QY 721 EV 722  
DB 721 EV 722

RESULT 4

AAH65063 PRELIMINARY; PRT; 722 AA.  
ID AAH65063  
AC AAH65063;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Delta-like 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



DR	InterPro; IPR000152; Asx_hydroxyl_S.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR006209; EGF_like.	
DR	Pfam; PF01414; DSL; 1.	
DR	Pfam; PF00008; EGF; 6.	
DR	PRINTS; PR00010; EGFBL00D.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.	
DR	PROSITE; PS00022; EGF_1; 8.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS00026; EGF_3; 7.	
DR	PROSITE; PS01187; EGF_CA; 2.	
KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein;	
KW	Repeat; Signal; Transmembrane.	
FT	SIGNAL 1 17 Potential.	
FT	CHAIN 18 722 Delta-like protein 1.	
FT	DOMAIN 18 545 Extracellular (Potential).	
FT	TRANSMEM 546 568 Potential.	
FT	DOMAIN 569 722 Cytoplasmic (Potential).	
FT	DOMAIN 158 220 DSL.	
FT	DOMAIN 225 253 EGF-like 1.	
FT	DOMAIN 256 284 EGF-like 2.	
FT	DOMAIN 291 324 EGF-like 3.	
FT	DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).	
FT	DOMAIN 369 401 EGF-like 5.	
FT	DOMAIN 408 439 EGF-like 6.	
FT	DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).	
FT	DOMAIN 484 515 EGF-like 8.	
FT	DISULFID 225 236 By similarity.	
FT	DISULFID 229 242 By similarity.	
FT	DISULFID 244 253 By similarity.	
FT	DISULFID 256 267 By similarity.	
FT	DISULFID 262 273 By similarity.	
FT	DISULFID 275 284 By similarity.	
FT	DISULFID 291 303 By similarity.	
FT	DISULFID 297 313 By similarity.	
FT	DISULFID 315 324 By similarity.	
FT	DISULFID 331 342 By similarity.	
FT	DISULFID 336 351 By similarity.	
FT	DISULFID 353 362 By similarity.	
FT	DISULFID 369 380 By similarity.	
FT	DISULFID 374 390 By similarity.	
FT	DISULFID 392 401 By similarity.	
FT	DISULFID 408 419 By similarity.	
FT	DISULFID 413 428 By similarity.	
FT	DISULFID 430 439 By similarity.	
FT	DISULFID 446 466 By similarity.	
FT	DISULFID 468 477 By similarity.	
FT	DISULFID 484 495 By similarity.	
FT	DISULFID 489 504 By similarity.	
FT	DISULFID 506 515 By similarity.	
FT	CARBOHYD 476 475 N-linked (GlcNAc...) (Potential).	
SQ	SEQUENCE 722 AA; 78448 MW; 95F581B56DCEC9B0 CRC64;	
Query Match 97.1%; Score 4003; DB 1; Length 722;		
Best Local Similarity 97.2%; Pred. No. 8.8e-269;		
Matches 702; Conservative 4; Mismatches 16; Indels 0; Gaps 0;		
QY	1 MGRRSALAVVSALLCQWSSGVFELKQEFVNNKGLGNRNCCRGSGPPCACRTFFR 60	
Db	1 MGRRSALAVVSALLCQWSSGVFELKQEFVNNKGLGNRNCCRGSGPPCACRTFFR 60	
QY	61 VCLKHYQASVSPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFTWPGTFS 120	
Db	61 VCLKHYQASVSPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFTWPGTFS 120	
QY	121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180	
Db	121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180	
QY	181 HYYGEGCSVFCRPDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240	

Db	181 HYYGEGCSVFCRPDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240	
QY	241 ECKCRVWGQGRYCDDECIRYPGCVHGTCCQWPQCQEGWGGLFCNQDLNYCTHHKPCRNG 300	
Db	241 ECKCRVWGQGRYCDDECIRYPGCVHGTCCQWPQCQEGWGGLFCNQDLNYCTHHKPCRNG 300	
QY	301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSFSCTCPGFGYK 360	
Db	301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAAPSPCKNGASCTDLEDSFSCTCPGFGYK 360	
QY	361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420	
Db	361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKMDLCGSSPCSNAGKCV 420	
QY	421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP 480	
Db	421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP 480	
QY	481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGPNQCQFLLPEPPPGPMVVDLSERHMESQG 540	
Db	481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGPNQCQFLLPEPPPGPMVVDLSERHMESQG 540	
QY	541 GPFPPWAVACGAVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGGCTETMNNLANCQREK 600	
Db	541 GPFPPWAVACGAVVLLVLLGCAAVVVCVRLKLOKHQPPPEPCGGGCTETMNNLANCQREK 600	
QY	601 DVSVSIIGATQIKNTNKKADFHDGHAKESSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660	
Db	601 DVSVSIIGATQIKNTNKKADFHDGHAKESSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660	
QY	661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720	
Db	661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720	
QY	721 EV 722.	
Db	721 EV 722.	

RESULT 6

DL11_RAT	STANDARD;	PRT;	714 AA.
ID	DL11_RAT		
AC	P97677;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).		
GN	Name=D11;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Disibio G., Hebshi L., Boulter J., Weinmaster G.;		
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: May be involved in cell-to-cell communication in		
CC	mammalian embryos. May have a role in cellular interactions		
CC	underlying somitogenesis and development of the nervous system (By		
CC	similarity).		
CC	-!- SUBUNIT: Interacts with Notch receptors.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- SIMILARITY: Contains 1 DSL domain.		
CC	-!- SIMILARITY: Contains 8 EGF-like domains.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		



CC	DR	EMBL; U78889; AAB37343.1; -.	-----	SQ	SEQUENCE	714 AA; 77378 MW; 488EE2272BAEA27E CRC64;	
DR	DR	HSSP; P08709; 1BF9.			Query Match	93.4%; Score 3848; DB 1; Length 714;	
DR	DR	RGD; 70949; D111.			Best Local Similarity	93.2%; Pred. No. 4.7e-258;	
DR	DR	GO; GO:0005576; C:extracellular; ISS.			Matches	673; Conservative 13; Mismatches 28; Indels 8; Gaps 1;	
DR	DR	GO; GO:0005887; C:integral to plasma membrane; ISS.		Qy	1	MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKGLGNRNCCRGSGPPCACRTFFR	60
DR	DR	GO; GO:0005112; F:Notch binding; IPI.		Db	1	MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKGLGNRNCCRGSGPPCACRTFFR	60
DR	DR	GO; GO:0030154; P:cell differentiation; ISS.		Qy	61	VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSPLDAGIDPAFSNPIRFPFGFTWPGTFS	120
DR	DR	GO; GO:0001709; P:cell fate determination; ISS.		Db	61	VCLKHYQASVSPEPPCTYGSATVPVLGVDSFSPLDAGIDPAFSNPIRFPFGFTWPGTFS	120
DR	DR	GO; GO:0009912; P:hair cell fate commitment; NAS.		Qy	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTLRLYSYRFVUDE	180
DR	DR	GO; GO:0030097; P:hemopoiesis; ISS.		Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTLRLYSYRFVUDE	180
DR	DR	GO; GO:0042472; P:inner ear morphogenesis; ISS.		Qy	181	HYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKGYCTDPICLPGCDDQHGYCDKPG	240
DR	DR	GO; GO:0007399; P:neurogenesis; NAS.		Db	181	HYGEGCSVFCRPRDDAFGHFTCGERGEKMDPGWKGYCTDPICLPGCDDQHGYCDKPG	240
DR	DR	GO; GO:0007219; P:Notch signaling pathway; NAS.		Qy	241	ECKCRVGWQGRYCDECIRYPCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG	300
DR	DR	GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.		Db	241	ECKCRVGWQGRYCDECIRYPCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG	300
DR	DR	GO; GO:0030155; P:regulation of cell adhesion; ISS.		Qy	301	ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSSFSCCTCPPGFYK	360
DR	DR	InterPro; IPR00152; Asx_hydroxyl_S.		Db	301	ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSSFSCCTCPPGFYK	360
DR	DR	InterPro; IPR00174; DSL.		Qy	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGENCEKMDLCGSSPSCNGAKCV	420
DR	DR	InterPro; IPR00742; EGF_2.		Db	361	VCELSAMTCADGPCFNGGRCSNPDGGYTCHCPLGFSGENCEKMDLCGSSPSCNGAKCV	420
DR	DR	InterPro; IPR001881; EGF_Ca.		Qy	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP	480
DR	DR	InterPro; IPR001438; EGF_II.		Db	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCAP	480
DR	DR	InterPro; IPR006209; EGF_like.		Qy	481	VSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLPPEPPGPMVVDLSERHMESQG	540
DR	DR	Pfam; PF01414; DSL; 1.		Db	481	VSRCEHAPCHNGATCHQRGORYMCECAQGYGGANCOFLPPEPPDLIVA-----AQG	532
DR	DR	Pfam; PF00008; EGF; 6.		Qy	541	GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQBPPEPCGGETETMNNLANCQREK	600
DR	DR	PRINTS; PR00010; EGFBLLOOD.		Db	533	GSFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLOKHQBPPEPCGGETETMNNLANCQREK	592
DR	DR	SMART; SM00051; DSL; 1.		Qy	601	DVSVSIIGATQIKNTNKKADFHDGDAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK	660
DR	DR	SMART; SM00179; EGF CA; 4.		Db	593	DVSVSIIGATQIKNTNKKADFHDGDAEKSSFKARYPTVDYNLIRDLKGDEATVRDAHSK	652
DR	DR	PROSITE; PS00010; ASX_HYDROXYL; 3.		Qy	661	RDTKCQSQSLOEKRRSPQHLGVGRFLTENRPESVYSTKDTKYQSVYVLSAEKDECVIAT	720
DR	DR	PROSITE; PS00022; EGF_1; 8.		Db	653	RDTKCQSQSGVGEKSTSLRGGEVDPDRKRPESVYSTKDTKYQSVYVLSAEKDECVIAT	712
DR	DR	PROSITE; PS01196; EGF_2; 8.		Qy	721	EV 722	
DR	DR	PROSITE; PS50026; EGF_3; 7.		Db	713	EV 714	
DR	DR	PROSITE; PS01187; EGF_CA; 2.					
KW	KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein;					
KW	KW	Repeat; Signal; Transmembrane.					
FT	FT	SIGNAL 1 17 Potential.					
FT	FT	CHAIN 18 714 Delta-like protein 1.					
FT	FT	DOMAIN 18 537 Extracellular (Potential).					
FT	FT	TRANSMEM 538 560 Potential.					
FT	FT	DOMAIN 561 714 Cytoplasmic (Potential).					
FT	FT	DOMAIN 158 220 DSL.					
FT	FT	DOMAIN 225 253 EGF-like 1.					
FT	FT	DOMAIN 256 284 EGF-like 2.					
FT	FT	DOMAIN 291 324 EGF-like 3.					
FT	FT	DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).					
FT	FT	DOMAIN 369 401 EGF-like 5.					
FT	FT	DOMAIN 408 439 EGF-like 6.					
FT	FT	DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).					
FT	FT	DOMAIN 484 515 EGF-like 8.					
FT	FT	DISULFID 225 236 By similarity.					
FT	FT	DISULFID 229 242 By similarity.					
FT	FT	DISULFID 244 253 By similarity.					
FT	FT	DISULFID 256 267 By similarity.					
FT	FT	DISULFID 262 273 By similarity.					
FT	FT	DISULFID 275 284 By similarity.					
FT	FT	DISULFID 291 303 By similarity.					
FT	FT	DISULFID 297 313 By similarity.					
FT	FT	DISULFID 315 324 By similarity.					
FT	FT	DISULFID 331 342 By similarity.					
FT	FT	DISULFID 336 351 By similarity.					
FT	FT	DISULFID 353 362 By similarity.					
FT	FT	DISULFID 369 380 By similarity.					
FT	FT	DISULFID 374 390 By similarity.					
FT	FT	DISULFID 392 401 By similarity.					
FT	FT	DISULFID 408 419 By similarity.					
FT	FT	DISULFID 413 428 By similarity.					
FT	FT	DISULFID 430 439 By similarity.					
FT	FT	DISULFID 446 466 By similarity.					
FT	FT	DISULFID 468 477 By similarity.					
FT	FT	DISULFID 484 495 By similarity.					
FT	FT	DISULFID 489 504 By similarity.					
FT	FT	DISULFID 506 515 By similarity.					
FT	FT	CARBOHYD 476 N-linked (GlcNAc. . .) (Potential).					

RESULT 7							
DL11_HUMAN	STANDARD;	PRT;	723 AA.				
ID DL11_HUMAN							
AC O00548; Q9NU41; Q9UJV2;							
DT 15-JUL-1998 (Rel. 36, Created)							
DT 15-JUL-1998 (Rel. 36, Last sequence update)							
DT 05-JUL-2004 (Rel. 44, Last annotation update)							
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal)							
DE (H-Delta-1) (UNQ146/PRO172).							
GN Name=DL11;							
OS Homo sapiens (Human).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
OX NCBI_TaxID=9606;							



RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=99180765; PubMed=10079256;  
RX Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;  
RT "Human ligands of the Notch receptor."  
RL Am. J. Pathol. 154:785-794(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Han W., Ye Q., Moore M.A.S.;  
RT "A soluble form of human delta-like-1 inhibits differentiation of  
hematopoietic progenitor cells."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Oda T., Chandrasekharappa S.C.;  
RT "Human Delta 1 gene sequence."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment."  
RL Genome Res. 13:2265-2270(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Almeida J.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP FUNCTION.  
RX MEDLINE=21464863; PubMed=11581320;  
RA Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,  
RA Henrique D., Parreira L.;  
RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human  
lymphoid differentiation."  
RL J. Exp. Med. 194:991-1001(2001).  
CC -!- FUNCTION: Acts as a ligand for Notch receptors. Blocks the  
differentiation of progenitor cells into the B-cell lineage while  
promoting the emergence of a population of cells with the  
characteristics of a T-cell/NK-cell precursor.  
CC -!- SUBUNIT: Interacts with Notch receptors.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower  
expression in brain and muscle and almost no expression in  
placenta, lung, liver, and kidney.  
CC -!- SIMILARITY: Contains 1 DSL domain.  
CC -!- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF003522; AAB61286.1; -.  
DR EMBL; AF196571; AAF05834.1; -.  
DR EMBL; AF222310; AAG09716.1; -.  
DR EMBL; AY358892; AAG89251.1; -.  
DR EMBL; AL078605; CAB89569.1; -.  
DR HSSP; P00740; 1EDM.  
DR Genew; HGNC:2908; DLL1.

DR MIM; 606582; -.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005112; F:Notch binding; IPI.  
DR GO; GO:0030154; P:cell differentiation; TAS.  
DR GO; GO:0001709; P:cell fate determination; NAS.  
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.  
DR GO; GO:0009912; P:hair cell fate commitment; ISS.  
DR GO; GO:0030097; P:hemoipoiesis; NAS.  
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.  
DR GO; GO:0007399; P:neurogenesis; ISS.  
DR GO; GO:0007219; P:Notch signaling pathway; NAS.  
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.  
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 7.  
DR PROSITE; PS01187; EGF\_CA; 1.  
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
KW Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 723 Delta-like protein 1.  
FT DOMAIN 18 545 Extracellular (Potential).  
FT TRANSMEM 546 568 Potential.  
FT DOMAIN 569 723 Cytoplasmic (Potential).  
FT DOMAIN 159 221 DSL.  
FT DOMAIN 226 254 EGF-like 1.  
FT DOMAIN 257 285 EGF-like 2.  
FT DOMAIN 292 325 EGF-like 3.  
FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).  
FT DOMAIN 370 402 EGF-like 5.  
FT DOMAIN 409 440 EGF-like 6.  
FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).  
FT DOMAIN 485 516 EGF-like 8.  
FT DISULFID 226 237 By similarity.  
FT DISULFID 230 243 By similarity.  
FT DISULFID 245 254 By similarity.  
FT DISULFID 257 268 By similarity.  
FT DISULFID 263 274 By similarity.  
FT DISULFID 276 285 By similarity.  
FT DISULFID 292 304 By similarity.  
FT DISULFID 298 314 By similarity.  
FT DISULFID 316 325 By similarity.  
FT DISULFID 332 343 By similarity.  
FT DISULFID 337 352 By similarity.  
FT DISULFID 354 363 By similarity.  
FT DISULFID 370 381 By similarity.  
FT DISULFID 375 391 By similarity.  
FT DISULFID 393 402 By similarity.  
FT DISULFID 409 420 By similarity.  
FT DISULFID 414 429 By similarity.  
FT DISULFID 431 440 By similarity.  
FT DISULFID 447 467 By similarity.  
FT DISULFID 469 478 By similarity.  
FT DISULFID 485 496 By similarity.  
FT DISULFID 490 505 By similarity.  
FT DISULFID 507 516 By similarity.  
FT CARBOHYD 477 477 N-linked (GlcNAc... ) (Potential).  
FT CONFLICT 498 498 E -> Q (in Ref. 2).  
FT CONFLICT 502 502 G -> R (in Ref. 4 and 5).  
FT CONFLICT 510 510 G -> S (in Ref. 2).

SQ	SEQUENCE	723 AA; 77956 MW; B4EC455FFA32A12B CRC64;	
	Query Match	88.6%; Score 3652.5; DB 1; Length 723;	
	Best Local Similarity	86.9%; Pred. No. 1.6e-244;	
	Matches	629; Conservative 46; Mismatches 46; Indels 3; Gaps 3;	
QY	1	MGRSALALAVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSG-PPCACRTFF	59
Db	1	MGRSALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFF	60
QY	60	RVCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTF	119
Db	61	RVCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGGGADSAFNSPIRFPFGFTWPGTF	120
QY	120	SLTIEALHTDSPDDLATENPERLISRLTQRLHTVGEWSQDLHSSGRTDLRYSYRFVCD	179
Db	121	SLTIEALHTDSPDDLATENPERLISRLTQRLHTVGEWSQDLHSSGRTDLKYSYRFVCD	180
QY	180	EHYVGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGOYCTDPICLPGCDDQHGYCDKP	239
Db	181	EHYVGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGYCTEPICLPGCDEQHGFCDKP	240
QY	240	GECKCRVWGQGRYCDDECIRYPCVHGTCQOPWQCNCQEGWGLFCNQDLNYCTHHKPCRN	299
Db	241	GECKCRVWGQGRYCDDECIRYPCGLHGTCCQOPWQCNCQEGWGLFCNQDLNYCTHHKPCQN	300
QY	300	GATCTNTGQSYTCSRCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSPSCTPPGFYG	359
Db	301	GATCTNTGQSYTCSRCRPGYTGATCELGIDECDDPSPCKNGGSCDTLENSYSCTCPPGFYG	360
QY	360	KVCELSAMTCADGPCFNGGRCSDNPDGGYTCCHCPLGFSGFNCEKMDLCGSSPSCNGAKC	419
Db	361	KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPSCNGAKC	420
QY	420	VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGVTGKNCSA	479
Db	421	VDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSCTCPGVTGRNCSA	480
QY	480	PVSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLLPEPPGPMVVDLSERHMESQ	539
Db	481	PVSRCEHAPCHNGATCHERGHYVCECARGYGGPNCQFLLPELPPGPAVVDLITEK-LEGO	539
QY	540	GGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQRE	599
Db	540	GGPFPWVAVCAGVILVLLLLGCAAVVVCVRLRLQKHRRPADPCRGETETMNNLANCQRE	599
QY	600	KDVSYSIIIGATQIKNTNKKADFHDGHAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS	659
Db	600	KDISYSIIIGATQIKNTNKKADFHDHADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHS	659
QY	660	KRDTKCQSQ-SLOEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI	718
Db	660	KRDTKCQPQSGSGEEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVI	719
QY	719	ATEV 722	
Db	720	ATEV 723	

RESULT 8  
Q90656  
ID Q90656 PRELIMINARY; PRT; 728 AA.  
AC Q90656;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE C-Delta-1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]

RP	SEQUENCE FROM N.A.	
RC	TISSUE=Spinal cord;	
RX	MEDLINE=95319507; PubMed=7596411;	
RA	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;	
RT	"Expression of a Delta homologue in prospective neurons in the	
RT	chick.";	
RL	Nature 375:787-790(1995).	
DR	EMBL; U26590; AAC59689.1; -.	
DR	PIR; I50719; I50719.	
DR	HSSP; P00740; IEDM.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0005509; F:calcium ion binding; IEA.	
DR	GO; GO:0007154; P:cell communication; IEA.	
DR	InterPro; IPR000152; Asx_hydroxyl_S.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR006209; EGF_like.	
DR	Pfam; PF01414; DSL; 1.	
DR	Pfam; PF00008; EGF; 6.	
DR	PRINTS; PR00010; EGFLOOD.	
DR	SMART; SM00051; DSL; 1.	
DR	SMART; SM00179; EGF_CA; 4.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.	
DR	PROSITE; PS00022; EGF_1; 8.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS50026; EGF_3; 6.	
DR	PROSITE; PS01187; EGF_CA; 2.	
KW	EGF-like domain.	
SQ	SEQUENCE 728 AA; 79861 MW; 93B2D6666D2388B7 CRC64;	
	Query Match	81.7%; Score 3368; DB 2; Length 728;
	Best Local Similarity	78.5%; Pred. No. 8.3e-225;
	Matches	574; Conservative 73; Mismatches 72; Indels 12; Gaps 6;
QY	1	MGRSALALAVVSALL--CQWSSGVFELKLQEFVNKKGLLGNRNCCRGSGP-----P 52
Db	1	MGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGQQQ 59
QY	53	CACRTFFRVCLKHQASVSPPEPCTYGSATPVLGVDSFSLPDGA-GIDPAFSNPIRFPF 111
Db	60	CDCKTFFRVCLKHQASVSPPEPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF 119
QY	112	GFTWPGTFSLLIEALHTDSPDDLATENPERLISRLTQRLHTVGEWSQDLHSSGRTDLR 171
Db	120	GFTWPGTFSLLIEALHTDSPDDLTTENPERLISRLTQRLHAVGEEWSQDLHSSGRTDLK 179
QY	172	YSYRFVCDEHYYGEGSVFCRPRDDAFGHFTCGDRGKMCDPGWKGOYCTDPICLPGCDD 231
Db	180	YSYRFVCDEHYYGEGSVFCRPRDDRFHFHTCGERGEKVCNPGWKGOYCTEPICLPGCDE 239
QY	232	QHGYCDKPGECKCRVWGQGRYCDDECIRYPCVHGTCQOPWQCNCQEGWGLFCNQDLNYC 291
Db	240	QHGFCDKPGECKCRVWGQGRYCDDECIRYPCGLHGTCCQOPWQCNCQEGWGLFCNQDLNYC 299
QY	292	THHKPCRNGATCTNTGQSYTCSRCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSPSC 351
Db	300	THHKPCRNGATCTNTGQSYTCSRCRPGYTGSSCEIINECDANPCKNGGSCDTLENSYSC 359
QY	352	TCPPGFYGVKVCELSAMTCADGPCFNGGRCSDNPDGGYTCCHCPLGFSGFNCEKXMDLCGSS 411
Db	360	TCPPGFYGVKNCELSAMTCADGPCFNGGRCCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419
QY	412	PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGG 471
Db	420	PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPFCVNGGTCQDGVNDYSCTCPGG 479
QY	472	YTGKNCSAPVSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNCQFLLPPEPPGPMVVDL 531
Db	480	YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGNLNCQFLLPPEPPGQPVIVDF 539
QY	532	SERHMESQGGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMN 591











DE	Hypothetical protein.	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RX	MEDLINE=2238257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Shevchenko Y., Bouffard G.G.,	
RA	Whiting M., Madan A., Young A.C., Rodriques S., Sanchez A.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RA	Strausberg R.;	
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC075742; AAH75742.1; -.	
KW	Hypothetical protein.	
SQ	SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;	
Query Match 67.4%; Score 2778; DB 2; Length 772;		
Best Local Similarity 62.3%; Pred. No. 6.3e-184;		
Matches 490; Conservative 87; Mismatches 131; Indels 78; Gaps 12;		
Qy	1 MGRSALAL-AVVSALLCQVWSSGVFELKLQEFVNKKGLGNRNCCRGG---SGPPCACR 56	
Db	1 MGRHLLLLFSILYMLLCCQASSGVFELKLQEFLNKKGVQGNKNCKGGLTTSYQQCECK 60	
Qy	57 TFRVCLKHYYQASVSEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWP 116	
Db	61 TFRICLKHYYQNASPEPPCTYGTVPVLGNSFQVPDILP-DGSFTNPIRMNFGFTWP 119	
Qy	117 GTFSLILIEALHTDSPDDLATENPERLISRLTTORHLTVGEWSDQLHSSGRTDLRYSYRF 176	
Db	120 GTFSLILIEALHADSKEDLTTFENPERIISTMTTQRLTVGEDWSQDLHVSGRTELKYSYRF 179	
Qy	177 VCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQYCTDPICLPGCDDQHGVC 236	
Db	180 VCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEIICDAGWKQYCTEPICLPGCDEEHGFC 239	
Qy	237 DKPGECKRQVWQGRYCDCEIRYPGCVHGTCCQPWQCNCQSGWGLFCNQDLNYCTHHKP 296	
Db	240 EKPGECKRQVGFKGRYCDECIRYPGLHGTCCQPWQCNCQSGWGLFCNQDLNYCTHHKP 299	
Qy	297 CRNGATCNTGQSYTCSRPGYTGANCELEVDCAVSPCKNGASCTDLEDSFSCTCPGG 356	
Db	300 CLNGATCNTGQSYTCSRPGFSGASCEIEVNECTGNPCNGSGCTDMENTYSCTCPGG 359	
Qy	357 FYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSFNCCKMDLCGSSPSCNG 416	
Db	360 FYGKNCELSAMTCADGPCFNGGRCADNPDGGYFCQCPYAGFNCCKIDHCSSSPSCNG 419	
Qy	417 AKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTKN 476	
Db	417 AKCVDLGNSYLCQCPDGFTGMNCDRAGDECSMYPQCGGTQCEGASGYMCTCPPGYTGRN 479	
Qy	477 CSAPVSRCEHAPCHNGATCHQQRQYMCCECAQGYGPNQCQFLLPPEPPGPMVVDLSERHM 536	
Db	480 CSSPVSRCQHNPCHNGATCHERNRNVYVCACVSGYGRNCQFLLPD-----RA 526	
Qy	537 ESQGGPFWPVAVCAGVVLVLLLLLGGCAAVVVCVRLKIQ--KHQPPPEPCGGETETMNNLA 594	
Db	527 SQIASDVPWTAVGSGVLLVLLLVACAVVVVCVRSKQQRRRDRDEVANGENETINNLT 586	
Qy	595 -NCQREKDVSVSIIGATQIKNTNKKADFGHDHG-----AEKSSFVRYPTVDYNLYRDLK 648	
Db	587 NNCHRDKOLAVSVVGVPVKNINKKIDFSSDHDLSLTTEKRSYKTRHAPADYNLVHEVK 646	
Qy	649 -----GDEATVRD--THSKRDTKCQ-----SQSLQEKRR-----SPOHLG 681	
Db	647 FEVKHEVKLEHAGKETTMANELSDCEDIKCQSLQDSSECTEKKRRRLKSDASEKSKYS 706	
Qy	682 VGRFLTENRPESVYSTK-----DTKYQSVYVLSAEKDEC 716	
Db	707 ESRYESKYESKYESKYSVDVSLYSESACASACASASTSACVDTKYKSVVMVMSSEKDEC 766	
Qy	717 VIATEV 722	
Db	767 VIATEV 772	
RESULT 14		
OS7462		
ID	OS7462	PRELIMINARY; PRT; 802 AA.
AC	OS7462;	
DT	01-JUN-1998 (Tremblrel. 06, Created)	
DT	01-JUN-1998 (Tremblrel. 06, Last sequence update)	
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)	
DE	DeltaA.	
GN	Name=dla; Synonyms=deltaA;	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98165392; PubMed=9425133;	
RA	Appel B., Eisen J.S.;	
RT	"Regulation of neuronal specification in the zebrafish spinal cord by	
RT	Delta function.";	
RL	Development 125:371-380(1998).	
DR	EMBL; AF030031; AAC41249.1; -.	
DR	HSSP; P00740; IEDM.	
DR	ZFIN; ZDB-GENE-980526-29; dla.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0005509; F:calcium ion binding; IEA.	
DR	GO; GO:0007154; P:cell communication; IEA.	
DR	InterPro; IPR000152; Asx_hydroxyl_s.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR006209; EGF_like.	
DR	Pfam; PF01414; DSL; 1.	
DR	Pfam; PF00008; EGF; 6.	
DR	PRINTS; PR00010; EGFBL00D.	
DR	SMART; SM00051; DSL; 1.	
DR	SMART; SM00179; EGF_CA; 3.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.	
DR	PROSITE; PS00022; EGF_1; 8.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS50026; EGF_3; 6.	
DR	PROSITE; PS01187; EGF_CA; 1.	
KW	EGF-like domain.	
SQ	SEQUENCE 802 AA; 88941 MW; 0D8A9734585918E5 CRC64;	



Db	105	IESWTNSAEQ-STENPDNLSRLATRRRLSIGEDWSQDIHLGQQSELRYSYHVSCDEHY	163
Qy	183	YGECSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGYCTDPICLPGCDDQHGYCDKPGEC	242
Db	164	YGDSCSDYCRPRDDNFGHYTCDEQGNRLCMSGWKGEYCAEPICLPGCSESHGFCELPGEC	223
Qy	243	KCRVGWQGRYCDICIRYPGCVHGTCCQPPWQCNQCEGWGGLFCNQDLNYCTHHKPCRNGAT	302
Db	224	KCRMWQGELECLRYPGCQHGSQCPWECICQEGWGGFLFCNQDLNYCTNHQPCRNGAS	283
Qy	303	CTNTGGSYTCSCRPGYTGANCELEWDECAPSPCKNGASCCTDLEDSFSCTCPPGFYGVKVC	362
Db	284	CINTGGSYS CSCRAGFTGTNCEIDINECASNPCKNGGSCNDLENDYECVCPRGFYKNC	343
Qy	363	ELSAMTCADGPCFNGGRCSDNPDG-GYTCHCPLGFSGFNCEKMKMDLCGSSPCSNGAKCVD	421
Db	344	DISAMTCEDGPCFNGGTCTIEKSSGVGVVCRPFNYHGSNCEKKIDRCTNSPCLNGGQCLD	403
Qy	422	LGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPV	481
Db	404	MGRNVLCRCRPGFSGPRCELNDDCASSPCANGGTCVDVANSYTCSTLGYGGKDCITLRV	463
Qy	482	SRCEHAPCHNGATCHQQRQRYMCECAQGYGGPNQCQLLPEPPPGPMVVDLSERHMESQGG	541
Db	464	DACSSKPCKNGGTCYTHFTGNVQCPTGFMGTSCFEFRVHDPTPASHRADSSNTLT-----	518
Qy	542	PPPWVAVCAGVVLVLLLLLGCAAVVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREKD	601
Db	519	-----MVVCLG--LTTFFLLGCGVFMV-MRGMRRGHFNEKGRVNDLEPKNNLI-----EKE	567
Qy	602	VSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKG---DEATVRDT	657
Db	568	-----PHFKMPNP-----DYLREKSSSKQKL-----LOGSESEEEERSGRT	603
Qy	658	HSKRDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSIVVLSAEKDECV	717
Db	604	DRKPDTK-----QCNPTSRY--PEDGAYHPIYIL-PEPEQCI	637
Qy	718	IATEV	722
Db	638	FATEV	642



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:11:34 ; Search time 60.7823 Seconds  
(without alignments)  
3411.281 Million cell updates/sec

Title: US-09-783-931-13  
Perfect score: 3383  
Sequence: 1 MGRLLASALLCVSGVFELKL.....DTKYQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	73.6	740	2 AAW00876	Aaw00876 C-Delta-1
2	2485.5	73.5	727	2 AAW11719	Aaw11719 C-Delta-1
3	2483	73.4	728	3 AAY79029	Aay79029 Chick del
4	2467	72.9	722	3 AAY79028	Aay79028 Murine de
5	2466	72.9	722	2 AAW11720	Aaw11720 M-Delta-1
6	2466	72.9	722	6 ABU55873	Abu55873 Mouse not
7	2466	72.9	722	6 AAE34029	Aae34029 Murine no
8	2401.5	71.0	723	2 AAW18353	Aaw18353 Prolifera
9	2401.5	71.0	723	2 AAW75492	Aaw75492 Human del
10	2401.5	71.0	723	2 AAW94498	Aaw94498 Human del
11	2401.5	71.0	723	3 AAY83227	Aay83227 PRO172 po
12	2401.5	71.0	723	3 AAB33422	Aab33422 Human PRO
13	2401.5	71.0	723	3 AAB24388	Aab24388 Human PRO
14	2401.5	71.0	723	3 AAY79032	Aay79032 Human del
15	2401.5	71.0	723	3 AAB00172	Aab00172 PRO172 po
16	2401.5	71.0	723	4 AAU12344	Aau12344 Human PRO
17	2401.5	71.0	723	4 AAB53064	Aab53064 Human ang
18	2401.5	71.0	723	6 ABO17788	Abol17788 Novel hum
19	2401.5	71.0	723	6 ABU81042	Abu81042 Human PRO
20	2401.5	71.0	723	6 ABP97824	Abp97824 Amino aci
21	2401.5	71.0	723	6 ABU66742	Abu66742 Human PRO
22	2401.5	71.0	723	6 ABU59823	Abu59823 Novel sec
23	2401.5	71.0	723	6 ABO25013	Abo25013 Human sec
24	2401.5	71.0	723	6 ABP72566	Abp72566 Human Not
25	2401.5	71.0	723	6 ABU67018	Abu67018 Human Not

26	2401.5	71.0	723	6 ADA45865	Ada45865 Novel hum
27	2401.5	71.0	723	6 ADA76296	Ada76296 Human PRO
28	2401.5	71.0	723	6 ADA18946	Ada18946 Human PRO
29	2401.5	71.0	723	6 ADA61569	Ada61569 Homo sapi
30	2401.5	71.0	723	6 ADB19354	Adb19354 Novel hum
31	2401.5	71.0	723	6 ADB27895	Adb27895 Human PRO
32	2401.5	71.0	723	6 ADA86374	Ada86374 Novel hum
33	2401.5	71.0	723	6 ADB15938	Adb15938 Human PRO
34	2401.5	71.0	723	6 ADA47724	Ada47724 Human PRO
35	2401.5	71.0	723	6 ADA67519	Ada67519 Human PRO
36	2401.5	71.0	723	6 ADB30526	Adb30526 Human PRO
37	2401.5	71.0	723	6 ADA85822	Ada85822 Novel hum
38	2401.5	71.0	723	6 ADA97034	Ada97034 Human PRO
39	2401.5	71.0	723	6 ADA79338	Ada79338 Human PRO
40	2401.5	71.0	723	6 ADA87477	Ada87477 Novel hum
41	2401.5	71.0	723	6 ADB16679	Adb16679 Human PRO
42	2401.5	71.0	723	6 ADA91771	Ada91771 Novel hum
43	2401.5	71.0	723	6 ADB14834	Adb14834 Human PRO
44	2401.5	71.0	723	6 ADB18795	Adb18795 Novel hum
45	2401.5	71.0	723	6 ADA94010	Ada94010 Human PRO

ALIGNMENTS

RESULT 1

AAW00876 AAW00876 standard; protein; 740 AA.

AC AAW00876;

DT 28-APR-1997 (first entry)

DE C-Delta-1 polypeptide (alternatively spliced variant).

KW C-Delta-1; cell proliferation; nervous system disorder;  
tissue regeneration; Notch; cervix cancer; breast cancer;  
colon cancer; melanoma; seminoma; neurogenesis; therapy.

OS Gallus sp.

FH Key Location/Qualifiers

FT Domain 184..228

FT Domain /label= DSL

FT Domain 229..261

FT Domain /label= EGF1

FT Domain 262..292

FT Domain /label= EGF2

FT Domain 293..332

FT Domain /label= EGF3

FT Domain 333..370

FT Domain /label= EGF4

FT Domain 371..409

FT Domain /label= EGF5

FT Domain 410..447

FT Domain /label= EGF6

FT Domain 448..485

FT Domain /label= EGF7

FT Domain 486..523

FT Domain /label= EGF8

FT Domain 524..534

FT Domain /label= EGF9

FT Domain 555..579

FT Domain /label= TM

FT /note= "transmembrane domain"

XX WO9701571-A1.

XX 16-JAN-1997.

PD 28-JUN-1996;

XX 96WO-US011178.

XX 28-JUN-1995;

PR 95US-0000589P.









Db 301 ATCTNTGQSGYTCSCRPYGTGANCELEVDCEDPSPCKNGASCTDLEQSFSCTCPGGFYGK 360

Qy 318 -CELSAMTCADGPCFNGRC-DNPDGG-YC-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367

Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYCRCPGLFGFNCEKKMDLGCSSPCNGAKCV 420

Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415

Db 421 DLGNSYLCRCQAGFGRYCFDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP 480

Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458

Db 481 VSRCEHAPCHNGATCHQQRQRYMCECAQYGGPNQFLLPEPPPGPMVVDLSERHMESQG 540

Qy 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503

Db 541 GPFPMWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGGCTETMNNLANCQREK 600

Qy 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540

Db 601 DVSVSIIGATQIKNTNKKADFGHDHGAKKSSFKVRYPTVDYNLVRLDKGDDATVRDTHSK 660

Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576

Db 661 RDTKCQSSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720

Qy 577 EV 578

Db 721 EV 722

RESULT 5

AAW11720

ID AAW11720 standard; protein; 722 AA.

XX

AC AAW11720;

DT 28-APR-1997 (first entry)

XX M-Delta-1 polypeptide.

DE M-Delta-1; cell proliferation; nervous system disorder;

XX tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;

KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

XX Mus sp.

XX WO9701571-A1.

XX 16-JAN-1997.

XX 28-JUN-1996; 96WO-US011178.

XX 28-JUN-1995; 95US-0000589P.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

PA (UYA ) UNIV YALE.

PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;

PI Gray GE;

XX WPI; 1997-100159/09.

DR N-PSDB; AAT58899.

XX New vertebrate Delta protein, DNA and antibodies - for treating and

PT preventing cancer, nervous system disorders and for tissue regeneration.

XX Claim 4; Fig 8; 135pp; English.

XX M-delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila

CC Delta, a protein that binds to Notch protein. It is expressed primarily

CC in presomitic mesoderm, the central and peripheral nervous systems, and

CC kidney. Chick (AAW11719) and human (AAW11721- 38) Delta-1 polypeptides

CC have also been identified. Delta-1 proteins can be used to treat or

CC prevent disorders characterised by increased Notch activity, such as

CC cervical, breast, lung or colon cancer, melanoma or seminoma, as well as

CC nervous system disorders, and to promote tissue regeneration and repair

XX

SQ Sequence 722 AA;

Query Match 72.9%; Score 2466; DB 2; Length 722;

Best Local Similarity 76.6%; Pred. No. 3.7e-112;

Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCCTFFR 45

Db 1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSPPCACRTFFR 60

Qy 46 VCLKHYQASVSPPEPCTYGSA-TPVLG--SFS-PDGAG-DPAFSPNIRPFPGFTWPGTFS 100

Db 61 VCLKHYQASVSPPEPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSPNIRPFPGFTWPGTFS 120

Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEESQDLHSSGRTDL-YSYRFVCFDE 156

Db 121 LIIEALHTDSPDDLATENPERLISRLTQRHLTVGEESQDLHSSGRTDLRYSYRFVCFDE 180

Qy 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKQOYCT-PICLPGC-DQHG-CDKPG 209

Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKQOYCTDPICLPGCDDQHGCDKPG 240

Qy 210 ECKCRVGMQGRYCDECIRYPGVHGTQOQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268

Db 241 ECKCRVGMQGRYCDECIRYPGCLHGTCQOQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300

Qy 269 ATCTNTGQSGYTCSCRPYGTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGGFYGK 317

Db 301 ATCTNTGQSGYTCSCRPYGTGANCELEVDCEAPSPCKNGASCTDLESFSCTCPGGFYGK 360

Qy 318 -CELSAMTCADGPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367

Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCPCPLGSGFNCEKKMDLGCSSPCNGAKCV 420

Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415

Db 421 DLGNSYLCRCQAGFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP 480

Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458

Db 481 VSRCEHAPCHNGATCHQQRQRYMCECAQYGGPNQFLLPEPPPGPMVVDLSERHMESQG 540

Qy 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503

Db 541 GPFPMWAVCAGVVLVLLLLGCAAVVVCVRLKQKHQPPPEPCGGGCTETMNNLANCQREK 600

Qy 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540

Db 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFKVRYPTVDYNLVRLDKGDEATVRDTHSK 660

Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576

Db 661 RDTKCQSSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720

Qy 577 EV 578

Db 721 EV 722

RESULT 6

ABU55873

ID ABU55873 standard; protein; 722 AA.

XX

AC ABU55873;

XX 25-MAR-2003 (first entry)

DE Mouse notch ligand delta-like 1 protein.

XX Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;  
KW ligand; Parkinson's disease; Huntington's disease; motor neuron disease;  
KW heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;  
KW acquired immunodeficiency syndrome.  
XX  
OS Mus sp.  
XX WO200277204-A2.  
PN  
XX  
PD 03-OCT-2002.  
XX  
XX 25-MAR-2002; 2002WO-GB001195.  
PF  
XX 23-MAR-2001; 2001GB-00007296.  
PR 23-MAR-2001; 2001GB-00007299.  
PR 17-APR-2001; 2001GB-00009346.  
XX  
PA (AXOR-) AXORDIA LTD.  
XX  
XX Andrews P, Walsh J, Gokhale P;  
PI  
XX  
DR WPI; 2003-092852/08.  
DR N-PSDB; ABX75296.  
XX  
PT Modulating the differentiation of embryonic stem cells by providing  
PT ligands which bind receptors in the Notch and Wnt pathways, useful for  
PT treating diseases such as Parkinson's, Huntington's, heart disease,  
PT diabetes and AIDS.  
XX  
PS Claim 6; Fig 3; 121pp; English.  
XX  
CC The invention relates to modulating the differentiation of an embryonic  
CC stem cell, comprising: (a) providing a culture of embryonic stem cells;  
CC (b) providing at least one ligand or its active binding fragment, capable  
CC of binding its cognate receptor polypeptide expressed by the embryonic  
CC stem cell; (c) forming a culture comprising embryonic stem cells and the  
CC ligand; and (d) growing the cell culture. Also included are: (1)  
CC Modulating the differentiation of embryonic stem cells, comprising: (a)  
CC providing a cell transfected with a nucleic acid molecule selected from:  
CC (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic  
CC acid molecule that hybridises to the nucleic acid in (i), and which  
CC encodes a ligand capable of modulating embryonic stem cell  
CC differentiation, or capable of binding a Wnt receptor; or (iii) nucleic  
CC acid molecules which are degenerate as a result of the genetic code to  
CC the sequences of (i) or (ii); (b) forming a culture comprising the cell  
CC identified in (a) with an embryonic stem cell; and (c) growing the  
CC culture for the maintenance and/or differentiation of the embryonic stem  
CC cell; (2) Inhibiting the differentiation of embryonic stem cells,  
CC comprising: (a) providing at least one polypeptide or its active  
CC fragment, that are inhibitors of the Wnt signalling pathway; (b) forming  
CC a culture comprising the cell identified in (a) with an embryonic stem  
CC cell; and (c) growing the culture for the maintenance of embryonic stem  
CC cells in an undifferentiated state; or (3) Inhibiting the differentiation  
CC of embryonic stem cells, comprising: (a) providing a cell transfected  
CC with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt  
CC inhibitory polypeptide; (ii) a molecule which hybridises to the molecule  
CC of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;  
CC and (iii) nucleic acid molecules which are degenerate as a result of the  
CC genetic code to the sequences of (i) or (ii); (b) forming a culture  
CC comprising the cell identified in (a) with an embryonic stem cell; and  
CC (c) growing the culture for the maintenance of embryonic stem cells in an  
CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture  
CC obtainable by any of the methods cited above. The therapeutic cell of the  
CC present invention is useful in the treatment of an animal, preferably a  
CC human, comprising administering a cell composition comprising embryonic  
CC stem cells which have been induced to differentiate into at least one  
CC cell-type. The cell is also useful for the manufacture of a composition  
CC for use in treatment of diseases such as Parkinson's disease,  
CC Huntington's disease, motor neuron disease, heart disease, diabetes,  
CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired  
CC immunodeficiency syndrome). The present sequence is represents a Wnt or  
CC Notch pathway protein (i.e. a ligand for the method of the invention)

XX SQ Sequence 722 AA;  
Query Match 72.9%; Score 2466; DB 6; Length 722;  
Best Local Similarity 76.6%; Pred. No. 3.7e-112;  
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;  
QY 1 MGR-----LLASALLC---VSGVFELKLEFVNKKGLL-NRNCCRGG-----GCCTFFR 45  
DB 1 MGRSALALAVVSALLCQWSSGVFELKLEFVNKKGLLGNRNCRCGGSGPPCACRTFFR 60  
QY 46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100  
DB 61 VCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180  
QY 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPGWKQYCTDPICLPGCDDQHGYCDKPG 240  
QY 210 ECKCRVWQGRYCDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268  
DB 241 ECKCRVWQGRYCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
QY 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPPGYVK 317  
DB 301 ATCTNTGQGSYTCSCRPGYTGANCELEVECAPSPCKNGASCTDLEDSEFSCCTCPPPGYVK 360  
QY 318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367  
DB 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGSGFNCEKKMDLCSSPSCSGAKCV 420  
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415  
DB 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVDFSCTCPGGYTGKNCSAP 480  
QY 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458  
DB 481 VSRCEHAPCHNGATCHQRGQRYMCECAQYGGPNCQFLLPEPPGPMVVDLSERHMESQG 540  
QY 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503  
DB 541 GPFPWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK 600  
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540  
DB 601 DVSVSIIGATQIKNTNKKADFHDHGAKKSSFKRYPTVDYNLVRDLKGDEATVRDTHSK 660  
QY 541 -----CSEEEKAL-----RKRPP-SVYSTSKDTKYQSVV--SEKDEC-IAT 576  
DB 661 RDTKCQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVVLSAEKDECVIAT 720  
QY 577 EV 578  
DB 721 EV 722  
RESULT 7  
AAE34029  
ID AAE34029 standard; protein; 722 AA.  
XX  
AC AAE34029;  
XX  
DT 02-MAY-2003 (first entry)  
XX  
DE Murine notch ligand delta-like 1 protein.  
XX  
KW Murine; drug screening; toxicology assay; signalling pathway;  
KW notch ligand delta-like 1.  
XX

OS Mus sp.  
XX WO200290992-A2.  
PN 14-NOV-2002.  
XX 29-APR-2002; 2002WO-GB001946.  
PF 04-MAY-2001; 2001GB-00011004.  
PR (AXOR-) AXORDIA LTD.  
XX Andrews P, Draper J, Walsh J;  
PI WPI; 2003-120579/11.  
DR N-PSDB; AAD52523.  
XX Identifying biologically active agents comprises cloning transfected  
PT cells into a cell array, exposing the array to an agent to be tested, and  
PT detecting signals generated by a reporter molecule as a result of  
PT exposure to the agent.  
XX Claim 16; Fig 2; 90pp; English.  
PS The present invention relates to a novel screening method which enables  
XX the identification of biologically active agents which mediate their  
CC effect through the activation of genes. The method involves providing a  
CC population of cells stably transfected with a nucleic acid encoding a  
CC reporter molecule, cloning the transfected cells into a cell array,  
CC exposing the array to at least one agent to be tested and detecting a  
CC signal generated by the reporter molecule as a result of exposure to the  
CC agent. The method is useful in identifying biologically active agents and  
CC the genes through which the agents act, in screening potential drugs for  
CC their ability to activate certain drug targets in a high-throughput  
CC assay, in identifying relationships between signalling pathways and  
CC specific signals that could be useful in eventually directing the  
CC differentiation of embryonic stem cells and in toxicology assays by  
CC testing for unwanted activation or inhibition of specific signalling  
CC pathways. The present sequence is murine notch ligand delta-like 1  
CC protein used to illustrate the method of the invention  
XX SQ Sequence 722 AA;  
Query Match 72.9%; Score 2466; DB 6; Length 722;  
Best Local Similarity 76.6%; Pred. No. 3.7e-112;  
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;  
QY 1 MGR-----LLASALLC---VSGVFELKLQEFVNNKGLL-NRNCRRGG-----GCCTFFR 45  
DB 1 MGRSALALAVVSALLCQVSSGVFELKLQEFVNNKGLLGNRNCRRGGSPPCACRTFFR 60  
QY 46 VCLKHYQASVSPEPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPGTFS 100  
DB 61 VCLKHYQASVSPEPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRPFPGFTWPGTFS 120  
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCD 156  
DB 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 180  
QY 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209  
DB 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGERKMDPGWKGOYCTDPICLPGCDDQHGCDKPG 240  
QY 210 ECKCRVGMQGRYDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268  
DB 241 ECKCRVGMQGRYDECIRYPGCLHGTCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
QY 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK 317  
DB 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFCTCPPGFYGK 360  
QY 318 -CELSAMTCADGCPFNNGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367  
|||||

Db 361 VCELSAMTCADGCPFNNGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLGGSSPCSNCAKCV 420  
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415  
|||||  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
QY 416 VSRCEH-PCHNGATCHRR---YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458  
|||||  
Db 481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGGPNCQFLLPEPPGPMVVDLSEHMSQG 540  
QY 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503  
|||||  
Db 541 GPFPMVAVCAGVVLVLLLLLGCAAVVVCVRLKIQKHQPPPEPCGGETETMNNLANCQREK 600  
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540  
|||||  
Db 601 DVSVSIIGATQIKNTNKKADFHDGAKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
QY 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576  
|||||  
Db 661 RDTKCQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
QY 577 EV 578  
||  
Db 721 EV 722  
RESULT 8  
AAW18353  
ID AAW18353 standard; protein; 723 AA.  
XX AAW18353;  
AC AAW18353;  
XX 11-FEB-1998 (first entry)  
DT Proliferation and differentiation suppression polypeptide.  
DE Proliferation; differentiation; suppression; human; delta-1; serrate-1;  
XX blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
KW Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /label= Signal  
FT Protein 22..723  
FT /label= Differentiation\_suppression\_protein  
XX WO9719172-A1.  
XX 29-MAY-1997.  
PD 15-NOV-1996; 96WO-JP003356.  
PF 17-NOV-1995; 95JP-00299611.  
PR 30-NOV-1995; 95JP-00311811.  
XX (ASAH ) ASahi Kasei Kogyo KK.  
XX Sakano S, Itoh A;  
PI WPI; 1997-298110/27.  
XX N-PSDB; AAT70174.  
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress  
PT proliferation and differentiation of undifferentiated human blood cells.  
XX Claim 15; Page 77-82; 114pp; Japanese.  
PS The present sequence represents a polypeptide which suppresses  
XX proliferation and differentiation of undifferentiated cells such as  
CC neurons and blood cells. The polypeptide may be used for the prevention  
CC and control of disorders involving undifferentiated cells, such as



CC leukaemia and malignant tumours, and improvement of blood formation, e.g.  
CC after immunosuppression  
XX  
SQ Sequence 723 AA;

Key	Location/Qualifiers
Peptide	1. .21
FT	/note= "signal peptide"
FT	22. .723
Protein	/note= "mature delta-1 protein"
FT	
FT	
XX	
PN	JP10316582-A.
XX	
PD	02-DEC-1998.
XX	
PF	14-MAY-1997; 97JP-00124062.
XX	
PR	14-MAY-1997; 97JP-00124062.
XX	
PA	(ASAH ) ASAHI KASEI KOGYO KK.
XX	
DR	WPI; 1999-076401/07.
DR	N-PSDB; AAX16817.
XX	
PT	Vascular cell controlling agent comprises polypeptide - which is human
PT	notch ligand and is used as drug.
XX	
PS	Disclosure; Page 16-19; 21pp; Japanese.
XX	
CC	This sequence represents the human delta-1 protein, which is a ligand of
CC	the human notch protein. The protein or fragments, especially AAW75493-
CC	W75495, can be used as a drug to control vascular cells. The sequences
CC	were isolated and the truncated fragments were generated using the
CC	primers AAX16818-X16831
XX	
SQ	Sequence 723 AA;



Db 553 ILVLMLLGCAAVVVCVRLRLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGGDTAVRDAHSKRDTKCQPOGSSG 672  
QY 543 EEKAL-----RKRPP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 673 EEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 10  
AAW94498  
ID AAW94498 standard; protein; 723 AA.  
XX  
AC AAW94498;  
XX  
DT 22-APR-1999 (first entry)  
XX  
DE Human delta-1 protein.  
XX

KW Human; delta-1; delta-2; differentiation inhibitor; proliferation;  
KW leukaemia; malignant tumour.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /label= signal  
FT Protein 22..723  
FT /label= Delta-1  
XX  
PN WO9851799-A1.

XX 19-NOV-1998.

PF 13-MAY-1998; 98WO-JP002104.

PR 14-MAY-1997; 97JP-00124064.

XX (ASAH ) ASAH KASEI KOGYO KK.

PI Sakano S;

XX WPI; 1999-070120/06.

DR N-PSDB; AAX16300.

XX Peptide inhibiting the differentiation of undifferentiated blood - used  
PT for treatment of cancer and other disorders and the culture of human  
PT cells in vitro.

XX Example 1; Page 64-69; 86pp; Japanese.

XX The present invention describes full length and shortened human delta-2  
CC proteins. Human delta-2 is a differentiation inhibitor which inhibits the  
CC differentiation of undifferentiated cells (other than brain or muscle  
CC cells), such as blood cells, and enhances the proliferation of  
CC undifferentiated blood cells. Products of human delta-2 may be used for  
CC the treatment of diseases such as leukaemia and malignant tumours. They  
CC may also be used in the culture of human cells in vitro, e.g. for  
CC production of supplies of undifferentiated blood cells. The present  
CC sequence represents human delta-1, from an example of the present  
CC invention

XX Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 2; Length 723;  
Best Local Similarity 75.1%; Pred. NO. 5e-109;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVS 56

Db 13 SALLCQVSSGVFELKLOEFVNKKGLLNRNCCRGAGPPPCACRTFFRVCLKHQASVS 72  
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFNPRIFFPGFTWPGTFSLIIEALHTDSP 111  
Db 73 PEPPCTYGSAVTPVLGVDSFSLPDGGADSAFNPRIFFPGFTWPGTFSLIIEALHTDSP 132  
QY 112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHYGEGSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDHYHYGEGSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPNPWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGR 252  
QY 221 YCDECIRYPGCVHGTCCQOPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YCDECIRYPGCLHGTCCQOPWQCNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312  
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFGYK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELIGIDECDPSPCKNGGSCDTLSENSYCTCPPGFGYKICELSAMTCAD 372  
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGSY-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSRCPCVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGTYGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTKLEGQGGPFPWAVCAGV 552  
QY 468 VL---LLLGCAG-VVCVRL---KQKPEC-----ETETMNNLANCQREK----SSIGATQI 512  
Db 553 ILVLMLLGCAAVVVCVRLRLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGGDTAVRDAHSKRDTKCQPOGSSG 672  
QY 543 EEKAL-----RKRPP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 673 EEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 11

AAW83227

ID AAW83227 standard; protein; 723 AA.

XX

AC AAW83227;

XX 16-AUG-2000 (first entry)

XX PRO172 Polypeptide.

XX Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;  
KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;  
KW leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.  
XX Homo sapiens.

OS

FH Key Location/Qualifiers

FT Peptide 1..21

FT /label= Signal\_peptide

FT Modified-site 2..8

FT /note= "N-myristoylation site"

FT Modified-site 37..43

FT /note= "N-myristoylation site"

FT Modified-site 40..46

FT /note= "N-myristoylation site"

FT Modified-site 93..97

FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		98. .104
FT	Modified-site	/note= "N-myristoylation site"
FT		99. .105
FT	Modified-site	/note= "N-myristoylation site"
FT		131. .135
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		154. .158
FT	Modified-site	/note= "Casein kinase II phosphorylation"
FT		176. .185
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT		203. .207
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		243. .255
FT	Domain	/label= EGF-like_domain
FT		252. .261
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT		262. .268
FT	Modified-site	/note= "N-myristoylation site"
FT		274. .286
FT	Domain	/note= "EGF-like domain"
FT		281. .287
FT	Modified-site	/note= "N-myristoylation site"
FT		282. .288
FT	Modified-site	/note= "N-myristoylation site"
FT		301. .307
FT	Modified-site	/note= "N-myristoylation site"
FT		310. .316
FT	Domain	/note= "N-myristoylation site"
FT		314. .326
FT	Domain	/label= EGF-like_domain
FT		328. .334
FT	Modified-site	/note= "N-myristoylation domain"
FT		340. .346
FT	Modified-site	/note= "N-myristoylation site"
FT		342. .346
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		343. .355
FT	Modified-site	/note= "Asn and Asp hydroxylation site"
FT		344. .348
FT	Domain	/note= "Casein kinase II phosphorylation site"
FT		352. .364
FT	Domain	/label= EGF-like_domain
FT		369. .373
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		378. .384
FT	Modified-site	/note= "N-myristoylation site"
FT		387. .393
FT	Modified-site	/note= "N-myristoylation site"
FT		391. .403
FT	Domain	/label= EGF-like_domain
FT		420. .432
FT	Modified-site	/note= "Asn and Asp hydroxylation site"
FT		429. .441
FT	Domain	/label= EGF-like_domain
FT		457. .461
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		458. .480
FT	Modified-site	/label= Asn and Asp hydroxylation site
FT		467. .479
FT	Domain	/label= EGF-like_domain
FT		477. .481
FT	Modified-site	/note= "N-glycosylation site"
FT		483. .487
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		495. .499
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT		505. .517
FT	Domain	/label= EGF-like_domain
FT		512. .518
FT	Modified-site	/note= "N-myristoylation site"
FT		548. .568
FT	Domain	/label= Transmembrane domain

FT	Binding-site	552. .563	/label= Prokaryotic membrane lipoprotein lipid attachment site
FT			
FT	Modified-site	659. .663	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	660. .664	/note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT	Modified-site	670. .674	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	671. .675	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	676. .682	/note= "N-myristoylation site"
FT	Modified-site	683. .689	/note= "N-myristoylation site"
FT	Modified-site	695. .701	/note= "N-myristoylation site"
FT	Modified-site	698. .702	/note= "Casein kinase II phosphorylation site"
XX			
FN	WO200021996-A2.		
XX	20-APR-2000.		
XX			
XX	05-OCT-1999;	99WO-US023089.	
XX	13-OCT-1998;	98US-0104080P.	
XX	(GETH ) GENENTECH INC.		
XX	Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI; Yuan J;		
XX			
DR	WPI; 2000-317943/27.		
DR	N-PSDB; AAZ93703.		
XX			
PT	Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.		
XX			
PS	Claim 12; Fig 8; 122pp; English.		
XX			
CC	Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia		
XX			
SQ	Sequence 723 AA;		
Query Match			
Best Local Similarity 71.0%; Score 2401.5; DB 3; Length 723;			
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67			
Qy	7	SALLC---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCCTFFRVCLKHYQASVS	56
Db	13	SALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGAGPPPCACRTFFRVCLKHYQASVS	72
Qy	57	PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPFRPFGTWPGTFSLIIEALHTDSP	111
Db	73	PEPPCTYGSAPVLGVDSFSLPDGGGADSAFNSNPIRPFPGTWPGTFSLIIEALHTDSP	132
Qy	112	DDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRIDL-YSYRFVCDHYHGGCSVFC	167
Db	133	DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRIDLKYSYRFVCDHYHGGCSVFC	192
Qy	168	RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR	220
Db	193	RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR	252
Qy	221	YCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY	279

Db 253 YCDECIRYPGCLHGTCCQPPQCNQCQEGWGLFCNQDLNYCTHHKPKNGATCTNTGQGSY 312

QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFGYK-CELSAMTCAD 327

Db 313 TCSCRPGYTGATCELGIDECDDPSPCKNGGSCDLENSYSCTCPPGFGYKICELSAMTCAD 372

QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK----DCSSPC-NGA-CVDLGNYS-C-CQ 376

Db 373 GPCFNGGRCSDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432

QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425

Db 433 AGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGTYTGRNCSAPVSRCEHAPCHN 492

QY 426 GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467

Db 493 GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWAVCAGV 552

QY 468 VL---LLLGCAA-VVCVRL---KQKEC-----ETETMNNLANCQREKD---SSIGATQI 512

Db 553 ILVLMLLLGCAAVVVCVRLRLQXHRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612

QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542

Db 613 KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPPQGSSG 672

QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578

Db 673 EEKGTPTTLRGGEASERKRDPDSCGSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 12

AAB33422

ID AAB33422 standard; protein; 723 AA.

XX AAB33422;

DT 29-JAN-2001 (first entry)

DE Human PRO172 protein UNQ146 SEQ ID NO:41.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.

XX Homo sapiens.

OS

XX WO200053758-A2.

PN

XX 14-SEP-2000.

PD

XX 02-MAR-2000; 2000WO-US005841.

PF

XX 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99US-0123618P.

PR 12-MAR-1999; 99US-0123957P.

PR 23-MAR-1999; 99US-0125775P.

PR 12-APR-1999; 99US-0128849P.

PR 20-APR-1999; 99WO-US008615.

PR 28-APR-1999; 99US-0131445P.

PR 04-MAY-1999; 99US-0132371P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-OCT-1999; 99US-0162506P.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

XX

PA (GETH ) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX

DR WPI; 2000-572271/53.

DR N-PSDB; AAC58587.

XX

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

PT

XX

PS Claim 33; Fig 18; 309pp; English.

XX

CC The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

XX

SQ Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;

Best Local Similarity 75.1%; Pred. No. 5e-109;

Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCRRG-----GCCTFFRVCLKHYSQSVS 56

Db 13 SALLCQVSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPACRTFFRVCLKHYSQASVS 72  
Qy 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLLIEALHTDSP 111  
Db 73 PEPPCTYGSAAVTPVLGVSFSLPDGGGADSAFNSNPIRFPFGFTWPGTFSLLIEALHTDSP 132  
Qy 112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTL-YSYRFVCDHEYHYGEGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTLKYSYRFVCDHEYHYGEGCSVFC 192  
Qy 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWGQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEHGFCDKPGECKCRVWGQGR 252  
Qy 221 YCDECIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YCDECIRYPGCLHGTCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312  
Qy 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGPFYGK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGPFYKICELSAMTCAD 372  
Qy 328 GPCFNGGRC-DNPDDGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSCRCPPVSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
Qy 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPGVTGRNCSAPVSRCEHAPCHN 492  
Qy 426 GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWVAVCAGV 552  
Qy 468 VL----LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREKD---SSIGATQI 512  
Db 553 ILVLMELLGCAAVVCVRLRLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
Qy 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDHSDKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPGSSG 672  
Qy 543 EEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 673 EEKGTPPTLRGGEASERKRDPDSCGSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 13  
AAB24388  
ID AAB24388 standard; protein; 723 AA.  
XX AC AAB24388;  
XX DT 07-NOV-2000 (first entry)  
XX DE Human PRO172 protein sequence SEQ ID NO:4.  
XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.  
XX OS Homo sapiens.  
XX WO200032221-A2.  
XX PN 08-JUN-2000.  
XX PD 30-NOV-1999; 99WO-US028313.  
XX PF 01-DEC-1998; 98WO-US025108.  
XX PR 16-DEC-1998; 98US-0112850P.

PR 12-JAN-1999; 99US-0115554P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-OCT-1999; 99US-0162506P.  
XX (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;  
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;  
PI Smith V, Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2000-412154/35.  
DR N-PSDB; AAA77512.  
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing  
PT and treating diagnosing a cardiovascular, endothelial or angiogenic  
PT disorders in mammals.  
XX Claim 72; Fig 2; 315pp; English.  
XX The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder in mammals by  
CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
CC and for identifying agonists and antagonists of these processes. The  
CC nucleic acids and the proteins they encode may be used in the prevention,  
CC treatment and diagnosis of diseases associated with inappropriate PRO  
CC expression such as cardiovascular, endothelial or angiogenic disorders in  
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For  
CC example, the nucleic acids (NCs) and vectors containing them and the PRO  
CC polypeptide may be used to treat disorders associated with decreased PRO  
CC expression. AAA77510 to AAA77721 and AAB244388 to AAB24435 represent  
CC nucleotide and protein sequences used in the exemplification of the  
XX present invention  
SQ Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;  
Best Local Similarity 75.1%; Pred. No. 5e-109;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy 7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCCRG-----GCCTFFRVCLKHYSQASVS 56  
Db 13 SALLCQVSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPACRTFFRVCLKHYSQASVS 72  
Qy 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLLIEALHTDSP 111  
Db 73 PEPPCTYGSAAVTPVLGVSFSLPDGGGADSAFNSNPIRFPFGFTWPGTFSLLIEALHTDSP 132  
Qy 112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTL-YSYRFVCDHEYHYGEGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTLKYSYRFVCDHEYHYGEGCSVFC 192  
Qy 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWGQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEHGFCDKPGECKCRVWGQGR 252  
Qy 221 YCDECIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YCDECIRYPGCLHGTCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312



QY 280 TCSRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYVK-CELSAMTCAD 327  
Db 313 TCSRPGYTGATCELGIDECDFSPCKNGGCTDLENSYSCTCPPGFYKICELSAMTCAD 372  
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSTCTPPGYTGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR----YCECA-GYGG-NCQFLLE-PPGP--VD----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLELPPGPAVVDLTEKLEGGGPPFWAVCAGV 552  
QY 468 VL---LLLCAA-VVCVRL---KQKPEC-----ETETMNLANCOREKD---SSIGATQI 512  
Db 553 ILVLMLLGCAAVVVCVRLRLQKRPADPCRGETETMNLANCOREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKC-----S 542  
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGGDTAVRDAHSKRDTKCPQGGSSG 672  
QY 543 EEKAL-----RKRPP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 673 EEKGTPTLRGEASERKRPPDSGCSSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 14  
AAV79032

ID AAV79032 standard; protein; 723 AA.

XX AAV79032;

DT 06-JUN-2000 (first entry)

XX Human delta protein amino acid sequence.

KW Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;  
KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;  
KW tissue regeneration; liver cirrhosis; keloid formation; baldness;  
KW inner ear disorder; human.

XX Homo sapiens.

PN WO200002897-A2.

XX 20-JAN-2000.

PF 13-JUL-1999; 99WO-US015817.

XX 13-JUL-1998; 98US-0092513P.

PR 19-OCT-1998; 98US-0104834P.

XX (UYYA ) UNIV YALE.

PI Artavanis-Tsakonas S, Rand MD, Qi H;

XX WPI; 2000-282852/24.

DR N-PSDB; AAZ98679.

XX New cleavage peptide, nucleic acids and antibodies useful for diagnosis,  
PT prevention and treatment of cancer, disorders of central nervous system,  
PT cirrhosis and psoriasis.

PS Claim 1; Fig 4; 177pp; English.

XX This sequence represents the human delta protein amino acid sequence.  
CC Delta is a toporythmic protein that contains a sequence which is cleaved  
CC by the metalloprotease-disintegrin Kuzbanian (Kuz). Cleavage by Kuz  
CC results in two fragments, a soluble amino terminal fragment consisting  
CC essentially of the extracellular domain, and a membrane bound fragment

CC consisting of the transmembrane domain and the intracellular domain. The  
CC soluble fragment is able to bind to Notch. Delta plays a key role in  
CC differentiation, and therefore detection and measurement of delta  
CC activation is important in the study of differentiation. The invention  
CC relates to the delta cleavage peptides (the active fragment), and to  
CC methods for detecting and measuring delta activation. Delta cleavage  
CC peptides, and chimeric proteins are useful for modulating the activity of  
CC Notch, delta or kuz or at least one of the signalling pathways in a cell  
CC or organism, expressing Notch. By contacting a cell with kuz protein or  
CC nucleic acid or its antibody, the activity or levels of delta protein is  
CC modulated and vice versa. A delta cleavage peptide or its derivative  
CC capable of binding kuz protein is useful for treating or preventing a  
CC disease or disorder associated with increased delta activity or  
CC expression such as cervical, breast, colon or lung cancer, melanoma or  
CC seminoma in humans. A recombinant cell comprising a delta peptide is  
CC useful for treating or preventing central nervous system disorders. A  
CC delta cleavage peptide is useful for the diagnosis of diseases or  
CC disorders associated with increased levels of Notch-delta protein binding  
CC activity comprising measuring the ability of delta cleavage peptides in a  
CC sample to bind kuz protein. A complex of delta protein and kuz is useful  
CC for diagnosing or screening for the presence of, or predisposition to  
CC developing a disease or disorder associated with aberrant levels of the  
CC complex, comprising measuring the level or functional activity of the  
CC complex or RNA encoding delta or kuz in a sample. The delta cleavage  
CC peptide is also useful for promoting tissue regeneration and repair, for  
CC treating liver cirrhosis, keloid formation, psoriasis, baldness and  
CC degenerative or traumatic disorders of the sensory epithelium of the  
CC inner ear

XX Sequence 723 AA;

QY Query Match 71.0%; Score 2401.5; DB 3; Length 723;  
Best Local Similarity 75.1%; Pred. No. 5e-109;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKLOEFVNKKGILL-NRNCRRGG-----GCCTFFRVCLKHYYQASVS 56  
Db 13 SALLCQVWSSGVFELKLOEFVNKKGILLNRNCRRGGAGPPCACRTFFRVCLKHYYQASVS 72  
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPPIRFPFGFTWPGTSLIIEALHTDSP 111  
Db 73 PEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFNSPIRFPFGFTWPGTSLIIEALHTDSP 132  
QY 112 DDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEHYGEGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHEHYGEGCSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGCD-QHG-CDKPGECKRVRGWQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKRVRGWQGR 252  
QY 221 YCDECIRYPGCVHGTCCQPPWCNQCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTQGGSY 279  
Db 253 YCDECIRYPGCLHGTCCQPPWCNQCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTQGGSY 312  
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYVK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELGIDECDFSPCKNGGCTDLENSYSCTCPPGFYKICELSAMTCAD 372  
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSCRCVPVYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSTCTPPGYTGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR----YCECA-GYGG-NCQFLLE-PPGP--VD----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHYVCECARGYGGPNCQFLLELPPGPAVVDLTEKLEGGGPPFWAVCAGV 552  
QY 468 VL---LLLCAA-VVCVRL---KQKPEC-----ETETMNLANCOREKD---SSIGATQI 512  
Db 553 ILVLMLLGCAAVVVCVRLRLQKRPADPCRGETETMNLANCOREKDISVSIIGATQI 612



XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;  
PI Yuan J;  
XX WPI; 2000-638201/61.  
DR N-PSDB; AAA54105.  
XX  
PT PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for  
PT treating tumors including cancers of the breast and lung, leukemia and  
PT for identifying compounds capable of inhibiting growth of neoplastic  
PT cells.  
XX  
PS Claim 31; Fig 8; 133pp; English.  
XX  
CC Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their  
CC agonists (preferably anti-PRO agonist antibody or a small molecule  
CC mimicking the biological activity of PRO polypeptide) are useful in vitro  
CC or in vivo for inhibiting the growth of a tumour cell. Compositions  
CC comprising the PRO polypeptides are useful for inhibiting neoplastic cell  
CC growth and for treating cancer including breast, ovarian, renal,  
CC colorectal, uterine, prostate, lung, bladder, central nervous system  
CC cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also  
CC useful for treating other disorders such as neuronal, glial, astrocytal,  
CC hypothalamic and other glandular, macrophagal, epithelial, stromal,  
CC blastocoealic disorders and inflammatory, angiogenic and immunologic  
CC disorders as well as being useful for identifying agonists to PRO  
CC polypeptides by contacting the polypeptide with a candidate molecule and  
CC monitoring biological activity mediated by the polypeptide  
XX  
SQ Sequence 723 AA;

Query Match 71.0%; Score 2401.5; DB 3; Length 723;  
Best Local Similarity 75.1%; Pred. No. 5e-109;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;  
QY 7 SALLC---VSGVFELKIQEFVNKKGLL-NRNCRRG-----GCCTFFRVCLKHQASVS 56  
Db 13 SALLCQWSSGVFELKIQEFVNKKGLLNRNCRRGGAGPPPCACRTFFRVCLKHQASVS 72  
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSPNIRFPFGFTWPGTFSLLIEALHTDSP 111  
Db 73 PEPPCTYGSATPVLGVDSFSLPDGGGADSAFSPNIRFPFGFTWPGTFSLLIEALHTDSP 132  
QY 112 DDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRVCDEHYGEGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRVCDEHYGEGCSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGCKCRVGMQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGCKCRVGMQGR 252  
QY 221 YCDECIRYPGCVHGTQQPWCNQCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YCDECIRYPGCLHGTQQPWCNQCQEGWGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312  
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLIES--SCTCPPGFYK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGFYKICELSAMTCAD 372  
QY 328 GPCFNNGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376  
Db 373 GPCFNNGRCSDSPDGGYSRCPCVYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDNVDCASSPCANGGTCTRDGVNDFSCPPGYTGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERHRYVCECARGYGGPNCQFLLPELPGPAVVDLTKLEGQGGFPWVAVCAGV 552

QY 468 VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREK-----SSIGATQI 512  
Db 553 ILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPPQGSSG 672  
QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 673 EEKGTPTTLRGGEASERKRPDSGCGSTSKDTKYQSVYVISEEKDECVIATEV 723

Search completed: November 29, 2004, 13:21:58  
Job time : 64.7823 secs

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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:18:13 ; Search time 16.1897 Seconds  
(without alignments)  
2367.669 Million cell updates/sec

Title: US-09-783-931-13  
Perfect score: 3383  
Sequence: 1 MGRLLASALLCVSGVFELKL.....DTKYQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3383	100.0	578	3 US-08-981-392-13	Sequence 13, Appl
2	3383	100.0	578	4 US-09-908-322-13	Sequence 13, Appl
3	2489	73.6	728	3 US-08-981-392-2	Sequence 2, Appli
4	2489	73.6	728	4 US-09-908-322-2	Sequence 2, Appli
5	2488.5	73.6	729	3 US-08-872-855-8	Sequence 8, Appli
6	2462	72.8	722	3 US-08-981-392-12	Sequence 12, Appl
7	2462	72.8	722	4 US-09-908-322-12	Sequence 12, Appl
8	2454	72.5	720	3 US-08-872-855-4	Sequence 4, Appli
9	2447.5	72.3	713	3 US-08-872-855-5	Sequence 5, Appli
10	2401.5	71.0	723	3 US-09-068-740A-9	Sequence 9, Appli
11	2401.5	71.0	723	4 US-09-423-753-27	Sequence 27, Appl
12	2401.5	71.0	723	4 US-10-140-002-346	Sequence 346, App
13	2390	70.6	702	3 US-09-068-740A-4	Sequence 4, Appli
14	2380.5	70.4	723	4 US-09-641-612-6	Sequence 6, Appli
15	2262.5	66.9	721	3 US-08-981-392-5	Sequence 5, Appli
16	2262.5	66.9	721	4 US-09-908-322-5	Sequence 5, Appli
17	2257.5	66.7	721	3 US-08-872-855-7	Sequence 7, Appli
18	2081.5	61.5	717	3 US-08-872-855-9	Sequence 9, Appli
19	2062.5	61.0	520	3 US-09-068-740A-3	Sequence 3, Appli
20	1378	40.7	642	3 US-08-872-855-10	Sequence 10, Appl
21	1329.5	39.3	659	4 US-09-423-753-3	Sequence 3, Appli
22	1329.5	39.3	685	3 US-08-872-855-2	Sequence 2, Appli
23	1329.5	39.3	685	4 US-09-423-753-25	Sequence 25, Appl
24	1329.5	39.3	685	4 US-09-641-612-7	Sequence 7, Appli
25	1329.5	39.3	685	4 US-10-140-002-88	Sequence 88, Appl
26	1192	35.2	500	4 US-09-423-753-2	Sequence 2, Appli
27	1086.5	32.1	833	1 US-08-264-534-6	Sequence 6, Appli

28	1086.5	32.1	833	1	US-08-083-590A-2	Sequence 2, Appli
29	1086.5	32.1	833	1	US-08-465-500-6	Sequence 6, Appli
30	1086.5	32.1	833	2	US-08-346-126-6	Sequence 6, Appli
31	1086.5	32.1	833	2	US-08-346-128-6	Sequence 6, Appli
32	1086.5	32.1	833	3	US-08-532-384-2	Sequence 2, Appli
33	1086.5	32.1	833	3	US-08-893-828-6	Sequence 6, Appli
34	1085.5	32.1	832	3	US-08-981-392-6	Sequence 6, Appli
35	1085.5	32.1	832	4	US-09-908-322-6	Sequence 6, Appli
36	1084.5	32.1	830	3	US-08-872-855-11	Sequence 11, Appl
37	993.5	29.4	276	3	US-08-981-392-43	Sequence 43, Appl
38	993.5	29.4	276	4	US-09-908-322-43	Sequence 43, Appl
39	968	28.6	1238	3	US-09-214-278-5	Sequence 5, Appli
40	968	28.6	1238	4	US-09-855-722-5	Sequence 5, Appli
41	965.5	28.5	1055	3	US-09-214-278-2	Sequence 2, Appli
42	965.5	28.5	1055	4	US-09-855-722-2	Sequence 2, Appli
43	965	28.5	192	3	US-08-981-392-65	Sequence 65, Appl
44	965	28.5	192	4	US-09-908-322-65	Sequence 65, Appl
45	964.5	28.5	1212	3	US-09-214-278-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-981-392-13  
; Sequence 13, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowitz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 578 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-981-392-13

Query Match 100.0%; Score 3383; DB 3; Length 578;  
Best Local Similarity 100.0%; Pred. No. 3.3e-245;  
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGRLLASALLCVSGVFELKQLQEFVNKKGLLNRCRGGGCTFFRVCLKHQASVSPEPP	60
Db	1		60
QY	61	CTYGSATPVLGSFSPDGAGDPAFSPNPIRFPFGFTWPGTFSLII EALHTDSPDDL	120
Db	61		120
QY	121	LISRLTORHLVGEEWSQDLHSSGRTDLYSYRFVFCDEHYHGGCSVFCRPRDDFGHFTCGR	180
Db	121		180
QY	181	GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVWGQGRYCDECIRYPGCVHGT	240
Db	181		240
QY	241	QCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSRPGYTGCEEECPCKNGS	300
Db	241		300
QY	301	CTDLESSCTCPPGFYGKCELSAMTCADGPCFNGGRCNDPDGGYCCPLGSGFNCEKKDCSS	360
Db	301		360
QY	361	PCNGACVDLGNISYCCQAGFGRCDNVDDCASPCNGGTCDVNDSTCPPPGYGNKNCSPVSRCE	420
Db	361		420
QY	421	HPCHNGATCHRRYCECAGYGGNCOFLLPEPPGPVDEEQFPWAVCAGLVLLLLGCAAVCV	480
Db	421		480
QY	481	RLKQKPECETETMNNLANCQREKDSIGATQIKNTNKKDFHDKKVRYPVDYNLVLKVHKK	540
Db	481		540
QY	541	CSEEKALRKRPVSYSTSKTKYQSVYVSEKDECIATEV	578
Db	541		578

## RESULT 2

US-09-908-322-13  
; Sequence 13, Application US/09908322  
; Patent No. 6783956  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
;
US-09-908-322-13
Query Match      100.0%; Score 3383; DB 4; Length 578;
Best Local Similarity 100.0%; Pred. No. 3.3e-245;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  MGRLLASALLCVSGVFELKLOEFVNKKGLLNRRNCCRGGCCTFFRVCLKHYYQASVSPEPP 60
Db      1  MGRLLASALLCVSGVFELKLOEFVNKKGLLNRRNCCRGGCCTFFRVCLKHYYQASVSPEPP 60

QY     61  CTYGSATPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTENPER 120
Db     61  CTYGSATPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTENPER 120

QY    121  LISRLTORHLVGEESQDLHSSGRTDLYSYRFVCDHYHYGEGCSVFCRPRDDFGHFTCGR 180
Db    121  LISRLTORHLVGEESQDLHSSGRTDLYSYRFVCDHYHYGEGCSVFCRPRDDFGHFTCGR 180

QY    181  GEKCPGWKGQYCTPICLPGCDQHGDCKPGECKCRVWGQRYCDECIRYPGCVHGTCCQPW 240
Db    181  GEKCPGWKGQYCTPICLPGCDQHGDCKPGECKCRVWGQRYCDECIRYPGCVHGTCCQPW 240

QY    241  QCNCQEGWGGLFCNQDNLNYCTHHKPCNGATCTNTGQSYTCSCRPGYTGCEEECPCKNGS 300
Db    241  QCNCQEGWGGLFCNQDNLNYCTHHKPCNGATCTNTGQSYTCSCRPGYTGCEEECPCKNGS 300

QY    301  CTDLESSCTPPGFYGKCELSAMTCADGPCFNGGRCNDNPDGGYCCPLGSGFNCEKKDCSS 360
Db    301  CTDLESSCTPPGFYGKCELSAMTCADGPCFNGGRCNDNPDGGYCCPLGSGFNCEKKDCSS 360

QY    361  PCNGACVDLGNISYCCQAGFGRCDNVDDCASPCNGGTCDVNDSDCTCPPGYGKNCSPVSRCE 420
Db    361  PCNGACVDLGNISYCCQAGFGRCDNVDDCASPCNGGTCDVNDSDCTCPPGYGKNCSPVSRCE 420

QY    421  HPCHNGATCHRRYCECAGYGGNCQFLPEPPGPVDEEQFPWAVCAGLVLLLLGCAAVVCV 480
Db    421  HPCHNGATCHRRYCECAGYGGNCQFLPEPPGPVDEEQFPWAVCAGLVLLLLGCAAVVCV 480

QY    481  RLKQKPECETETMNNLANCQREKDSISIGATQIKNTNKKDFHDKKVRYPVDYNLVLKVHKK 540
Db    481  RLKQKPECETETMNNLANCQREKDSISIGATQIKNTNKKDFHDKKVRYPVDYNLVLKVHKK 540

QY    541  CSEKALRKRPVSYSTSKDTKYQSVYVSEKDECIATEV 578
Db    541  CSEKALRKRPVSYSTSKDTKYQSVYVSEKDECIATEV 578

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### RESULT 3

US-08-981-392-2  
; Sequence 2, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace

```
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-392-2

Query Match 73.6%; Score 2489; DB 3; Length 728;
Best Local Similarity 76.0%; Pred. No. 3.4e-178;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

QY 5 LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCRRGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCRGGGPGAGQQQCDCKTFFRVCL 70

QY 49 KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGTFSLI 102
Db 71 KHYQASVSPEPPCTYGSATPVLGANSFSVPDGAGADPAFSNPIRFPFGFTWPGTFSLI 130

QY 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHY 158
Db 131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDHY 190

QY 159 YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211
Db 191 YGEGCSVFCRPRDRFRGHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQHGFCDKPGEC 250

QY 212 KCRVGMQGRYCDECIRYPCGVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGAT 270
Db 251 KCRVGMQGRYCDECIRYPCGLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCNGAT 310

QY 271 CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
Db 311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCNKGSGCTDLENSYCTCPPGFYGKNC 370

QY 319 ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
Db 371 ELSAMTCADGPCFNGGRCITDNPDDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDL 430

QY 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417
Db 431 GNSYICQCAQAGFTGRHCDNDVDDCASFPVNGGTGQDGVNDYSCTCPPGYNGKNCSPTVS 490

QY 418 RCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPP-GPV-----DEEQ 458
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Db 491 RCEHNPCHNGATCHERSNRVYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGQNSQ 550
QY 459 FPW-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCQREKD- 504
Db 551 FPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKDI 610
QY 505 --SSIGATQIKNTKK-DPH-----DK---KVRYP-VDYNLVLKV-----HKKC--- 541
Db 611 SISVIGATQIKNTKKVDFHSDNSDKNGYKVRYPVDYNLVHELKNEGSVKEEHGKCEAK 670
QY 542 -----SEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578
Db 671 CETYDSEAEKSAVQLKSSDTSERKRDPDSVYSTSKDTKYQSVYVISEEKDECIATEV 728

RESULT 4
US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2
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Query Match 73.6%; Score 2489; DB 4; Length 728;
Best Local Similarity 76.0%; Pred. No. 3.4e-178;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

QY 5 LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCRRGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCRGGGPGAGQQQCDCKTFFRVCL 70
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US-09-908-322-12

Query Match 72.8%; Score 2462; DB 4; Length 722;  
Best Local Similarity 75.9%; Pred. No. 3.5e-176;  
Matches 548; Conservative 6; Mismatches 24; Indels 14

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Db		:	
Db	1	MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSGGSPCACRTFFR	60
QY	46	VCLKHYQASVSPEPPCTYGSA--TPVLG--SFS-PDGAG-DPAFNSPIRFPFGFTWPGTFS	100
Db			
Db	61	VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFNSPIRFPFGFTWPGTFS	120
QY	101	LIIEALHTDSPDDL--TENPERLISRL--TORHL--VGEWSQDLHSSGRTDL--YSYRFVVCDE	156
Db			
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVVCDE	180
QY	157	HYYGEGCSVFCRPRDD--FGHFTCG--RGEK--C--PGWKQOYCT--PICLPGC--DQHG--CDKPG	209
Db			
Db	181	HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGCDKPG	240
QY	210	ECKCRVWQGRYCDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC--NG	268
Db			
Db	241	ECKCRVWQGRYCDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRN	300
QY	269	ATCTNTGQSYTCSCRPGYTG--CE--EEC--PCXNG--SCTDLES--SCTCPPGFGYK	317
Db			
Db	301	ATCTNTGQSYTCSCRPGYTGANCELEVEDCAPSPCKNGASCTDLEDSFSCTCPPGFGYK	360
QY	318	-CELSAMTCADGPCFNGGRC--DNPDSGY--C--CPLG--SGFNCEKKD--C--SSPC--NGA--CV	367
Db			
Db	361	VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCSSSPCSNGAKCV	420
QY	368	DLGNSY--C--CQAGF--GR--C--DNVDDCA--SPC--NGGTC--DVND--SCTCPGY--GKNCS--P	415
Db			
Db	421	DLGNSYLCRCQAGFGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPGYTGKNCSAP	480
QY	416	VSRCEH--PCHNGATCHRR-----YCECA--GYGG--NCQFLLPE--PPGP--VD-----EEQ-	458
Db			
Db	481	VSRCEHAPCHNGATCHQRGORYMCECAQYGGPNCFLLPEPPPGPMVVDLSERHMESQG	540
QY	459	--FPW--AVCAGLV---LLLLGCAA--VVCVRLK--QK-----PE--C--ETETMNNLANCQREK	503
Db			
Db	541	GPFPWVAVCAGVLVLLLLLGCAAVVVVCVRLKLQKHQPPPEPCGGGTEETMNNLANCQREK	600
QY	504	D---SSIGATQIKNTNKK--DFHDK-----KVRYP--VDYNLV-----LK	536
Db			
Db	601	DVSVSIIIGATQIKNTNKKADFHDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK	660
QY	537	VHKKCEEKALRKR-----PSVYSTSKDTKYQSVYV--SEKDEC--IAT	576
Db		:	
Db	661	RDTKCQSOSLOEKRRSPQHVGVRFLTENRPESVYSTSKDTKYQSVVLSAEKDECVIAT	720
QY	577	EV	578
Db			
Db	721	EV	722

## RESULT 8

US-08-872-855-4  
; Sequence 4, Application US/08872855  
; Patent No. 6121045  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND  
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston

Db 600 VSVIIIGATQIKNTNKKADPHGDHGAKKSSFVRYPTVDYNLVRDLKGD EATVRDTHSKR 659  
QY 541 -----CSEKAL-----RKR P-SVYSTSKDTKYQSVYV--SEKDEC-IATE 577  
Db 660 DTKQSQSSAGEEKIAPT LRGGEIPDRKR PESVYSTSKDTKYQSVYVLSAEKDECVIATE 719  
QY 578 V 578  
Db 720 V 720

RESULT 9

US-08-872-855-5  
; Sequence 5, Application US/08872855  
; Patent No. 6121045  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND  
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,855  
; FILING DATE: 11-JUN-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MAA-003.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-872-855-5

Query Match 72.3%; Score 2447.5; DB 3; Length 713;  
Best Local Similarity 75.7%; Pred. No. 4.2e-175;  
Matches 540; Conservative 9; Mismatches 29; Indels 135; Gaps 66;

QY 1 MGR-----LLSALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTFFR 45  
Db 1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR 60  
QY 46 VCLKHYQASVSPEPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPGTFS 100  
Db 61 VCLKHYQASVSPEPCTYGS AVTAVLGVDSFSLPDGAGIDPAFSNPIRPFPGFTWPGTFS 120  
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHLVGEEWSQDLHSSGRTDL-YSYRFVCD E 157  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHTVGEEWSQDLHSSGRTDLYSYRFVCD E 180  
QY 158 YYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG E 210  
Db 181 YYGEGCSVFCRPRDDAFGHFTCGERGEKMDPGWKGOYCTDPICLPGCDDQHG YCDKPG E 240

QY 211 CKCRVWGQGRYCD ECI RYPGCVHGT CQQPWQCNQCBGWGGLFCNQDLNYCTHHKPC-NGA 269  
Db 241 CKCRVWGQGRYCD ECI RYPGCLHGT CQQPWQCNQCBGWGGLFCNQDLNYCTHHKPCRNGA 300  
QY 270 TCTNTGQGSYTCSCRPGYT G--CE---EEC---PCKN-GSCTDLES--SCTCPPGFY GK- 317  
Db 301 TCTNTGQGSYTCSCRPGYT GANCELEVEDECAPSCKNGGSC TDLEDYSYCTCPPGFY GKV 360  
QY 318 CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVD 368  
Db 361 CELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCS SSPCSNGAKCVD 420  
QY 369 LGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PV 416  
Db 421 LGNSYLCRCQTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPV 480  
QY 417 SRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPPGPV----DEEQFW-AVC 464  
Db 481 SRCEHAPCHNGATCHQRGQRYMCECAQGYGGANGQFLLPEPPD LIVA AQGGSFPWAVC 540  
QY 465 AGLV---LLLLGCAA-VVCVRLK---QKP--EC--ETETMNNLANCQREK D---SSIGA 509  
Db 541 AGVVLVLLLLLGCAA VVVCVRLK LQKHQPPDP CGGETETMNNLANCQREKDVSVSIIGA 600  
QY 510 TQIKNTNKK-DFH-----DK---KVRYP-VDYNLV--LK-----VHKK----- 540  
Db 601 TQIKNTNKKADFHGDHGA DKS SFKARYPTVDYNLIRDLKGDEATVRDAHSKRDTKCQSQG 660  
QY 541 -CSEKAL-----RKR P-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 661 SAGEEKSTSTLRGGEVPDRKR PESVYSTSKDTKYQSVYVLSAEKDECVIATEV 713

RESULT 10

US-09-068-740A-9  
; Sequence 9, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-068-740A-9

Query Match 71.0%; Score 2401.5; DB 3; Length 723;  
Best Local Similarity 75.1%; Pred. No. 1.2e-171;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTFFR VCLKHYQASVS 56  
Db 13 SALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGAGPPPCACRTFFR VCLKHYQASVS 72  
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPGTFS LIIEALHTDSP 111  
Db 73 PEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSNPIRPFPGFTWPGTFS LIIEALHTDSP 132  
QY 112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCD EHYVGECSVFC 167

Db 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHYGEGCSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGR 252  
QY 221 YDECI RYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YDECI RYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312  
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGFYGKICELSAMTCAD 372  
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSCRCPPVYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSCTCPGYTGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGGGPPFWAVCAGV 552  
QY 468 VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREKD---SSIGATQI 512  
Db 553 ILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRTDKCQPGSSG 672  
QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578  
Db 673 EEKGTPTTLRGGEASERKRPDSCSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 11

US-09-423-753-27  
; Sequence 27, Application US/09423753  
; Patent No. 6664098  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR  
; FILE REFERENCE: KP-8693  
; CURRENT APPLICATION NUMBER: US/09/423,753  
; CURRENT FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: PCT/JF98/02104  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 9/124064  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-753-27

Query Match 71.0%; Score 2401.5; DB 4; Length 723;  
Best Local Similarity 75.1%; Pred. No. 1.2e-171;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;  
QY 7 SALLC---VSGVFELKLOEFVNKKGLL-NRNCCRGG-----GCCTFFRVCLKHQASVS 56  
Db 13 SALLCQVWSSGVFELKLOEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVCLKHQASVS 72  
QY 57 PEPPTYGSA-TPVLG--SFS-PDGAG-DPAFNSPIRPFPGFTWPGTFSLLIIEALHTDSP 111  
Db 73 PEPPTYGSAVTPVLGVDSFSLPDGGGADSAFNSPIRPFPGFTWPGTFSLLIIEALHTDSP 132

QY 112 DDL-TENPERLISRL-TORHL-VGEWSQDLHSSGRTDL-YSYRFVCDHYHYGEGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHYGEGCSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWQGR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGR 252  
QY 221 YDECI RYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YDECI RYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312  
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327  
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGFYGKICELSAMTCAD 372  
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376  
Db 373 GPCFNGGRCSDSPDGGYSCRCPPVYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432  
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425  
Db 433 AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSCTCPGYTGRNCSAPVSRCEHAPCHN 492  
QY 426 GATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467  
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGGGPPFWAVCAGV 552  
QY 468 VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREKD---SSIGATQI 512  
Db 553 ILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612  
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542  
Db 613 KNTNKKADFHGDSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRTDKCQPGSSG 672  
QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578  
Db 673 EEKGTPTTLRGGEASERKRPDSCSTSKDTKYQSVYVISEEKDECVIATEV 723

RESULT 12

US-10-140-002-346  
; Sequence 346, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT



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; ORGANISM: Homo Sapien
US-10-140-002-346

Query Match      71.0%; Score 2401.5; DB 4; Length 723;
Best Local Similarity 75.1%; Pred. No. 1.2e-171;
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

QY 7 SALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVS 56
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13 SALLCQWSSGVFELKLOEFVNKKGLLGNRNCRRGGAGPPPCACRTFFRVCLKHQASVS 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPPIRPFPGFTWPGTFSLLIEALHTDSP 111
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 PEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPPIRPFPGFTWPGTFSLLIEALHTDSP 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHGGCSVFC 167
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133 DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDHYHGGCSVFC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKRVGWQGR 220
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKRVGWQGR 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 221 YDECIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 YDECIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCKNMGATCTNTGQGSY 312
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCDLENSYSCTCPPGFYGKICELSAMTCAD 372
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQ 376
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 GPCFNGGRCSDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSCTPPGYTGGRNCSAPVSRCEHAPCHN 492
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 426 GATCHRR----YCECA-GYGG-NCQFLLE-PPGP--VD-----EEQ---FPW-AVCAGL 467
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 493 GATCHERGHRYVCECARGYGGPNCQFLLELPPGPVAVVDLLEKLEGGGGPFPVAVCAGV 552
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 468 VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREK-----SSIGATQI 512
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 553 ILVLMLLLGCAAUVVVCVRLRLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQI 612
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 613 KNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCPQGGSSG 672
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 543 EEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 673 EEKGTPTTLRGGEASERKRDPDSCGSTSKDTKYQSVYVISEEKDECVIATEV 723
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-068-740A-4
; Sequence 4, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
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; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-068-740A-4

Query Match      70.6%; Score 2390; DB 3; Length 702;
Best Local Similarity 75.4%; Pred. No. 8.2e-171;
Matches 529; Conservative 11; Mismatches 26; Indels 136; Gaps 66;

QY 13 SGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVSPEPCTYGS 65
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SGVFELKLOEFVNKKGLLGNRNCRRGGAGPPPCACRTFFRVCLKHQASVSPEPCTYGS 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 66 A-TPVLG--SFS-PDGAG-DPAFSNPPIRPFPGFTWPGTFSLLIEALHTDSPDDL-TENPE 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AVTPVLGVDSFSLPDGGGADSAFSNPPIRPFPGFTWPGTFSLLIEALHTDSPDLATENPE 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 120 RLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHGGCSVFCRPRDD-FGH 175
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 RLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDHYHGGCSVFCRPRDDAFGH 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 176 FTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKRVGWQGRYCDDECIRYP 229
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 FTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKRVGWQGRYCDDECIRYP 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 230 GCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPGYT 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GCLHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCKNMGATCTNTGQGSYTCSCRPGYT 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 G--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCADGCFNGGRC 336
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 301 GATCELGIDECDPSPCKNGGSCDLENSYSCTCPPGFYGKICELSAMTCADGCFNGGRC 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 337 -DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYSY-C-CQAGF-GR-C- 382
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 361 SDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 383 DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHNGATCHRR-- 432
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 DNVDDCASSPCANGGTCRDGVNDFSCTPPGYTGGRNCSAPVSRCEHAPCHNGATCHERGH 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 --YCECA-GYGG-NCQFLLE-PPGP--VD-----EEQ---FPW-AVCAGLVL---LLLG 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 RYVCECARGYGGPNCQFLLELPPGPVAVVDLLEKLEGGGGPFPVAVCAGVILVLMLLLG 540
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 CAA-VVCVRL---KQKPEC-----ETETMNNLANCQREK---SSIGATQIKNTNKK-DF 520
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 CAAVVVCVRLRLQKRRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADF 600
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 521 H-----DK---KVRYP-VDYNLV-----LKVHKKC-----SEEKAL----- 547
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 HGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCPQGGSSGEEKGTPPTTL 660
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

548 -----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
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661 RGGEASERKRDPDSCGSTSKDTKYQSVYVISEEKDECVIATEV 702
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RESULT 14
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6

Query Match      70.4%; Score 2380.5; DB 4; Length 723;
Best Local Similarity 74.7%; Pred. No. 4.4e-170;
Matches 531; Conservative 11; Mismatches 30; Indels 139; Gaps 67;

QY      7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHQASVS 56
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Db      13 SALLCQVSSGVFELKLQEFVNKKGLLGNPNCCRGAGPPPCACRTFFRVCLKHQASVS 72

QY      57 PEPPTCYGSA-TPVLG--SFS-PDGAG-DPAFSPNPIRPFPGFTWPGTFSLIIEALHTDSP 111
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Db      73 PEPPTCYGSAVTPVLGVDSFSLPDGGGADSAFSPNPIRPFPGFTWPGTFSLIIEALHTDSP 132

QY      112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHYGEGSVFC 167
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      133 DDLATENPERLISPLATORHLTVGEEWSQDLHSSGRTDLKYSYRFVCDHYHYGEGSVFC 192

QY      168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVWGQR 220
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Db      193 RPDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGDEQHGFCDKPGECKCRVWGQR 252

QY      221 YDDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      253 YDDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312

QY      280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      313 TCSCRPGYTGATGELGIDEDPSPCKNGGSCDTLENSYSCTCPGFGYKICELSAMTCAD 372

QY      328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFENCEK--DCSSPC-NGA-CVDLGNYS-C-CQ 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      373 GPCFNGGRCSDSPDGGYSCRCVPVSGFENCEKKIDYCSSPSCSNGAKCVDLGDAYLCRCQ 432

QY      377 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGY-GKNCS-PVSRCEH-PCHN 425
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Db      433 AGFSGRHCDNDVDDCASSPCANGGTCRDGVNDFSCTCPGYTGRNCSAPVSRCEHAPCHN 492

QY      426 GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL 467
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Db      493 GATCHERGHYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWAVCAGV 552

QY      468 VL---LLLGCAA-VVCVRL---KQPEC-----ETETMNNLANCQREK----SSIGATQI 512
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QY      513 KNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC-----S 542
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Db      613 KNTNKKADFHDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPGQSSG 672

QY      543 EEKAL-----RKR-SPVYSTSKDTKYQSVVY--SEKDEC-IATEV 578
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Db      673 EEKGTPTTLRGGEASERKRDPDSGCSSTSKDTKYQSVYVVISSEKDECVIATEV 723

RESULT 15
US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-5

Query Match      66.9%; Score 2262.5; DB 3; Length 721;
Best Local Similarity 68.7%; Pred. No. 2.9e-161;
Matches 489; Conservative 39; Mismatches 47; Indels 137; Gaps 61;

QY      4 LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCRRGG-----CCTFFRVCLKH 51
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Db      10 LVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCRRPGSLASLQRCCEKTFFRICLKH 69

QY      52 QASVSPEPPCTYGSA-TPVLGSFS--PDGA-GDPAFSPNPIRPFPGFTWPGTFSLIIEAL 106
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      70 QSNVSPEPPCTYGGAVTPVLGTSFVVPPESSNADPTFSNPIRPFPGFTWPGTFSLIIEAI 129

QY      107 HTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHYGEG 162
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      130 HADSADDLNTENPERLISRLATORHLTVGEQWSQDLHSSDRTELKYSYRFVCDHYHYGEG 189

QY      163 CSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCDQHG--CDKPGECKCRV 215
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      190 CSDYCRPRDDAFGHFSCGEKGEKLCNPGWKGLYCTEPICLPGCDEHHGYCDKPGECKCRV 249

QY      216 GWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNT 274
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Db      250 GWQGRYCDECIRYPGCLHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPCENGATCTNT 309

QY      275 GQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLESS--CTCPPGFYGK-CELSA 322
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Db      310 GQGSYTCSCRPGYTGSGNCEIEVNECDANPCKNKGSGSCDLENSYTCSCPPGFYGNCELSA 369

QY      323 MTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFENCEK--DCSS-PC-NGA-CVDLGNYS 373
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Db      370 MTCADGPCFNGGRCADNPDGGYICFCVPVGYSGFENCEKKIDYCSSNPCANGARCEDLGNYS 429

QY      374 CQQA--GF-GR-C-DNVDDCAS-PC-NGGTC--VND-SCTCPGY-GKNCS-PVSRCEH 421
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      430 ICQCEGFSGRNCDNLDLDDCTSFPCQNGGTCQDQINDYSCTCPGYIGKNCSMPITKCEH 489

QY      422 -PCHNGATCHRR----YCECA-GYGG-NCQFLLP-BPPGPVD-----EEQFPW-AV 463
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      490 NPCHNGATCHERNRNYVQCARGYGNNCQFLLPEKPVVVDLTEKYTEGSGQFPWIAV 549

QY      464 CAGLVL---LLLGCAA-VVCVRL-----KQPEC-----ETETMNNLANCQREK----SSIG 508
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QY 509 ATQIKNTNKK-DF-----HDKKVRY-VDYNLV-----LKVHKKCS--- 542  
Db 610 TTQIKNTNKKIDFLSESNNKNGYKPRYPSPVDYNLVHELKVEDSPKEERSKCEAKCSSND 669  
QY 543 -----EEKALRKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578  
Db 670 SDSVDVNSVHSKRDSSERRRPPDSAYSTSKDTKYQSVVVISDEKDECIATEV 721

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Job time : 19.1897 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2004, 13:26:20 ; Search time 58.226 Seconds  
(without alignments)  
3520.994 Million cell updates/sec

Title: US-09-783-931-13  
Perfect score: 3383  
Sequence: 1 MGRLLASALLCVGVFELKL.....DTKYQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62  
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Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2489	73.6	728	9	US-09-783-931-13
4	2489	73.6	728	10	US-09-783-931-13
5	2488.5	73.6	729	14	US-10-417-719-8
6	2466	72.9	722	15	US-10-417-719-8
7	2466	72.9	722	16	US-10-417-719-8
8	2462	72.8	722	9	US-09-783-931-12
9	2462	72.8	722	10	US-09-783-931-12
10	2454	72.5	720	14	US-10-417-719-4
11	2447.5	72.3	713	14	US-10-417-719-5
12	2436	72.0	714	15	US-10-417-719-5
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15	2401.5	71.0	723	14	US-10-028-072-346	Sequence 346, App
16	2401.5	71.0	723	14	US-10-140-808-346	Sequence 346, App
17	2401.5	71.0	723	14	US-10-121-049-346	Sequence 346, App
18	2401.5	71.0	723	14	US-10-123-904-346	Sequence 346, App
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22	2401.5	71.0	723	14	US-10-176-921-346	Sequence 346, App
23	2401.5	71.0	723	14	US-10-137-865-346	Sequence 346, App
24	2401.5	71.0	723	14	US-10-140-474-346	Sequence 346, App
25	2401.5	71.0	723	14	US-10-142-431-346	Sequence 346, App
26	2401.5	71.0	723	14	US-10-143-114-346	Sequence 346, App
27	2401.5	71.0	723	14	US-10-140-002-346	Sequence 346, App
28	2401.5	71.0	723	14	US-10-142-419-346	Sequence 346, App
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30	2401.5	71.0	723	14	US-10-123-262-346	Sequence 346, App
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42	2401.5	71.0	723	14	US-10-123-903-346	Sequence 346, App
43	2401.5	71.0	723	14	US-10-124-819-346	Sequence 346, App
44	2401.5	71.0	723	14	US-10-124-822-346	Sequence 346, App
45	2401.5	71.0	723	14	US-10-140-925-346	Sequence 346, App

ALIGNMENTS

RESULT 1  
US-09-908-322-13  
; Sequence 13, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowitz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-908-322-13

Query Match      100.0%; Score 3383; DB 9; Length 578;
Best Local Similarity 100.0%; Pred. No. 3e-238;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGRLLASALLCVSGVFELKLOEFVNKKGLLRNCCRGSGCCTFFRVCLKHYQASVSP 60
QY 61 CTYGSATPVLGSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIIEALHTDSPDDL 120
Db 61 CTYGSATPVLGSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIIEALHTDSPDDL 120
QY 121 LISRLTQRHLVGEWSQDLHSSGRTDLYSYRFVCDHEYHGGCVFCRPRDDFGH 180
Db 121 LISRLTQRHLVGEWSQDLHSSGRTDLYSYRFVCDHEYHGGCVFCRPRDDFGH 180
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QY 241 QCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSCRPGYTGC 300
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RESULT 2

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US-09-783-931-13
; Sequence 13, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-783-931-13
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Query Match      100.0%; Score 3383; DB 10; Length 578;
Best Local Similarity 100.0%; Pred. No. 3e-238;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLASALLCVSGVFELKLOEFVNKKGLLRNCCRGSGCCTFFRVCLKHYQASVSP 60
Db 1 MGRLLASALLCVSGVFELKLOEFVNKKGLLRNCCRGSGCCTFFRVCLKHYQASVSP 60
QY 61 CTYGSATPVLGSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIIEALHTDSPDDL 120
Db 61 CTYGSATPVLGSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIIEALHTDSPDDL 120
QY 121 LISRLTQRHLVGEWSQDLHSSGRTDLYSYRFVCDHEYHGGCVFCRPRDDFGH 180
Db 121 LISRLTQRHLVGEWSQDLHSSGRTDLYSYRFVCDHEYHGGCVFCRPRDDFGH 180
QY 181 GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVWGQGRYCDICIRYPGCV 240
Db 181 GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVWGQGRYCDICIRYPGCV 240
QY 241 QCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSCRPGYTGC 300
Db 241 QCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQSYTCSCRPGYTGC 300
QY 301 CTDLESSCTCPPGFYGKCELSAMTCADGPCFNGGRCNDPDGGYCCPLGSGFN 360
Db 301 CTDLESSCTCPPGFYGKCELSAMTCADGPCFNGGRCNDPDGGYCCPLGSGFN 360
QY 361 PCNGACVDLGNISYCCQAGFGRCDNVDDCASPNGGTCVNDSTCTPPGYGKNC 420
Db 361 PCNGACVDLGNISYCCQAGFGRCDNVDDCASPNGGTCVNDSTCTPPGYGKNC 420
QY 421 HPCNMGATCHRRYCECAGYGNCCQFLLPEPPGPVDEEQPWAACAGLVLL 480
Db 421 HPCNMGATCHRRYCECAGYGNCCQFLLPEPPGPVDEEQPWAACAGLVLL 480
QY 481 RLKQKPECETETMNNLANCQREKDSIGATQIKNTNKKDFHDKKVRYPVDYN 540
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Db 481 RLKQKECETETMNNLANCOREKDSIGATQIKNTNKKDFHDKVRYPDVYNLVKVK 540  
QY 541 CSEKALRKRPVSYSTSKTKYQSVYVSEKDECIATEV 578  
Db 541 CSEKALRKRPVSYSTSKTKYQSVYVSEKDECIATEV 578  
RESULT 3  
US-09-908-322-2  
; Sequence 2, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 728 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-908-322-2  
Query Match 73.6%; Score 2489; DB 9; Length 728;  
Best Local Similarity 76.0%; Pred. NO. 5.6e-173;  
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;  
QY 5 LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCRRGG-----CCTFFRVCL 48  
Db 11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCRGGPGGAGQQQCDCKTFFRVCL 70  
QY 49 KHYQASVSEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGTFSLI 102  
Db 71 KHYQASVSEPPCTYGSAITPVLGANSFSVPDGAGADPAFSNPIRFPFGFTWPGTFSLI 130  
QY 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEY 158  
Db 131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKYSYRFVCDHEY 190

QY 159 YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211  
Db 191 YGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEHQFCDKPGEC 250  
QY 212 KCRVWQGRYCDCEIRYPGCVHGTCCQOPWQCQEGWGLFCNQDLNYCTHHKPC-NGAT 270  
Db 251 KCRVWQGRYCDCEIRYPGCLHGTCCQOPWQCQEGWGLFCNQDLNYCTHHKPCNGAT 310  
QY 271 CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPGPGYK-C 318  
Db 311 CTNTGQGSYTCSCRPGYTGSSECEIEINECDANPCNGGSCDTLENSYCTCPGPGYGNK 370  
QY 319 ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369  
Db 371 ELSAMTCADGPCFNGGRC-TDNDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDL 430  
QY 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417  
Db 431 GNSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCDQDGVNDYSCTCPPGYNGKNCSTPVS 490  
QY 418 RCEH-PCHNGATCHRR---YCECA-GYGG-NCQFLLPEPP-GPV-----DEEQ 458  
Db 491 RCEHNPCHNGATCHERSNRYVCECARGYGLNCQFLLPEPPQGPVIVDFTEKYTEGQNSQ 550  
QY 459 FPW-AVCAGLVL---LLLGCAG-VVCVRLK-----QKPEC---ETETMNNLANCQREKD- 504  
Db 551 FPWIAVCAGIILVLMLLGCAAIVVCVRLKVQRHHQPEACRSETETMNNLANCQREKDI 610  
QY 505 --SSIGATQIKNTNKK-DFH----DK---KVRYP-VDYNLVLVK-----HKKC--- 541  
Db 611 SISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSPVDYNLVHELKNEDSVKBEHGKCEAK 670  
QY 542 -----SEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578  
Db 671 CETYDSEAEKSAVQLKSSDTSERKRPSVYSTSKDTKYQSVYVISEEKDECIATEV 728  
RESULT 4  
US-09-783-931-2  
; Sequence 2, Application US/09783931  
; Publication No. US20030073620A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; AND FRAGMENTS  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/783,931  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605

```
;
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-931-2

Query Match      73.6%; Score 2489; DB 10; Length 728;
Best Local Similarity 76.0%; Pred. No. 5.6e-173;
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

Qy 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRCGGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQQQCDCKTFFRVCL 70

Qy 49 KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGFSLI 102
Db 71 KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGFSLI 130

Qy 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHY 158
Db 131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDHY 190

Qy 159 YGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGCD-QHG-CDKPGEC 211
Db 191 YGEGSVFCRPRDDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQHGFCDKPGEC 250

Qy 212 KCRVWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGAT 270
Db 251 KCRVWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCTHHKPCXNGAT 310

Qy 271 CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
Db 311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGSGCTDLENSYSCTCPPGFYGNKC 370

Qy 319 ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSSPC-NGA-CVDL 369
Db 371 ELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCEKKIDYCSSSPCANGAQCVDL 430

Qy 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417
Db 431 GNSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCCQDGVNDYSCTCPPGYNGKNCSTPVS 490

Qy 418 RCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPP-GPV-----DEEQ 458
Db 491 RCEHNPCHNGATCHERSNRYVCBCARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGQNSQ 550

Qy 459 FPM-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCOREKD- 504
Db 551 FPMIACVAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCOREKDI 610

Qy 505 --SSIGATQIKNTKK-DFH----DK--KVRYP-VDYNLVLKV-----HKKC--- 541
Db 611 SISVIGATQIKNTKKVDFHSDNSDKNGYKVRYPVDYNLVLHKLKNEDSVKEEHGKCEAK 670

Qy 542 -----SEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
Db 671 CETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIATEV 728

RESULT 5
US-10-417-719-8
; Sequence 8, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
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```
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Gallus Gallus
US-10-417-719-8

Query Match      73.6%; Score 2488.5; DB 14; Length 729;
Best Local Similarity 75.9%; Pred. No. 6.1e-173;
Matches 546; Conservative 9; Mismatches 19; Indels 145; Gaps 65;

Qy 5 LASALLC-----VSGVFELKLOEFVNKKGLL-NRNCRCGGG-----CCTFFRVCL 48
Db 11 LLSALLCRCQVDGSGVFELKLOEFVNKKGLLSNRNCRCGGPGGAGQQQCDCKTFFRVCL 70

Qy 49 KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGFSLI 102
Db 71 KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGFSLI 130

Qy 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHY 158
Db 131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDHY 190

Qy 159 YGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGCD-QHG-CDKPGEC 211
Db 191 YGEGSVFCRPRDDRFGHFTCGERGEKVCNPGWKGOYCTEPICLPGCDEQHGFCDKPGEC 250

Qy 212 KCRVWQGRYCDECIRYPGCVHGTCCQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGAT 270
Db 251 KCRVWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCTHHKPCXNGAT 310

Qy 271 CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
Db 311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGSGCTDLENSYSCTCPPGFYGNKC 370

Qy 319 ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSSPC-NG--ACVD 368
Db 371 ELSAMTCADGPCFNGGRCCTDNPDGYSRCRPLGYSGFNCEKKIDYCSSSPCANGAQCVD 430

Qy 369 LGNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PV 416
Db 431 LGNSYICQCQAGFTGRHCDNDVDDCASFPVCVNGGTCCQDGVNDYSCTCPPGYNGKNCSTPV 490

Qy 417 SRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPP-GPV-----DEE 457
Db 491 SRCEHNPCHNGATCHERSNRYVCBCARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGQNS 550

Qy 458 QPPW-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCOREKD 504
Db 551 QPPWIAVCAGIILVLMLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCOREKD 610

Qy 505 ---SSIGATQIKNTKK-DFH----DK--KVRYP-VDYNLVLKV-----HKKC-- 541
Db 611 ISISVIGATQIKNTKKVDFHSDNSDKNGYKVRYPVDYNLVLHKLKNEDSVKEEHGKCEA 670

Qy 542 -----SEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
Db 671 KCETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIATEV 729
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RESULT 6
US-10-042-865-107
; Sequence 107, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-107

Query Match      72.9%; Score 2466; DB 15; Length 722;
Best Local Similarity 76.6%; Pred. No. 2.6e-171;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY      1 MGR-----LLASALIC---VSGVFELKLQEFVNKKGLL-NRNCRRGG-----GCCTFFR 45
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Db      1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSGSGPPCARTFFR 60
QY      46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGTWPGTFS 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGTWPGTFS 120
QY      101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180
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QY      157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKQYCTDPICLPGCDDQHGCDKPG 240
QY      210 ECKCRVGWQGRYCDECIRYPGCVHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 ECKCRVGWQGRYCDECIRYPGCLHGTCCQWPQCNCQEGWGLFCNQDLNYCTHHKPCRN 300
QY      269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNNG-SCITDLES--SCTCPPGFY 317
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFCTCPPGFY 360
QY      318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCLGFSGFNCEKKMDLCSGSSPCSNGAKCV 420
QY      368 DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGY-GKNCS-P 415
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP 480
QY      416 VSRCEH-PCNGATCHRR---YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 VSRCEHAPCHNGATCHQGRQYMCECAQYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 540
QY      459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNLANCOREK 503
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      541 GPFPMVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNLANCOREK 600
QY      504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      601 DVSVSIIGATQIKNTNKKADFHDGHDGAKKSSFKVRYPTVDYNLVRDLGDEATVRDTHSK 660
QY      541 -----CSEKAL-----RKRPP-SVYSTSKOTKYQSVV--SEKDEC-IAT 576
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      661 RDTKCQSSSAGEEKIAPTLRGGEIPDRKRPPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
QY      577 EV 578
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Db      721 EV 722
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RESULT 7
US-10-731-741-4
; Sequence 4, Application US/10731741
; Publication No. US20040171148A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt, Thomas M.
; APPLICANT: Zuniga-Pflucker, Juan-Carlos
; TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell
; TITLE OF INVENTION: Lineage and Methods of Making and Using Them
; FILE REFERENCE: 2223-171
; CURRENT APPLICATION NUMBER: US/10/731,741
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432,525
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-731-741-4
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Query Match      72.9%; Score 2466; DB 16; Length 722;
Best Local Similarity 76.6%; Pred. No. 2.6e-171;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY      1 MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCRRGG-----GCCTFFR 45
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Db      1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGSGSGPPCARTFFR 60
QY      46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGTWPGTFS 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180
```

Db 61 VCLKHYQASVSEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCD 156  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFV 180  
Qy 157 HYYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209  
Db 181 HYYGEGSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240  
Qy 210 ECKCRVWGQGRYCD 156  
Db 241 ECKCRVWGQGRYCD 156  
Qy 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFGY 317  
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVD 360  
Qy 318 -CELSAMTCADGPGCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367  
Db 361 VCELSAMTCADGPGCFNGGRCSDNPDGGYTCHCPLGSGFNCEKKMDLCGSSPCSN 420  
Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480  
Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458  
Db 481 VSRCEHAPCHNGATCHORQORYMCECAQYGGPNQCFLPPEPPGPMVVDLSERHME 540  
Qy 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANC 503  
Db 541 GPFPWAVACAGVVLVLLLLLGCAA-VVCVRLKQKHQPPPEPCGGETETMNNLANC 600  
Qy 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540  
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGA 660  
Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576  
Db 661 RDTKQSQSSAGEEKIAPTLRGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDEC 720  
Qy 577 EV 578  
Db 721 EV 722

RESULT 8

US-09-908-322-12  
; Sequence 12, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; City: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 722 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-908-322-12

Query Match 72.8%; Score 2462; DB 9; Length 722;  
Best Local Similarity 75.9%; Pred. No. 5.2e-171;  
Matches 548; Conservative 6; Mismatches 24; Indels 144; Gaps 68;

Qy 1 MGR-----LLASALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFFR 45  
Db 1 MGRSALALAVVSALLCQWSSGVFELKLOEFVNKKGLLGNRNCRRGGSGPPCACRFFR 60  
Qy 46 VCLKHYQASVSEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100  
Db 61 VCLKHYQASVSEPPCTYGSATPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120  
Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCD 156  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 180  
Qy 157 HYYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209  
Db 181 HYYGEGSVFCRPRDDAFGHFTCGDRGKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240  
Qy 210 ECKCRVWGQGRYCD 156  
Db 241 ECKCRVWGQGRYCD 156  
Qy 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFGY 317  
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVD 360  
Qy 318 -CELSAMTCADGPGCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367  
Db 361 VCELSAMTCADGPGCFNGGRCSDNPDGGYTCHCPLGSGFNCEKKMDLCGSSPCSN 420  
Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC 480  
Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458  
Db 481 VSRCEHAPCHNGATCHORQORYMCECAQYGGPNQCFLPPEPPGPMVVDLSERHME 540  
Qy 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANC 503  
Db 541 GPFPWAVACAGVVLVLLLLLGCAA-VVCVRLKQKHQPPPEPCGGETETMNNLANC 600  
Qy 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 536  
Db 601 DVSVSIIGATQIKNTNKKADFHGDHGA 660

QY 537 VHKCSEKALRKR-----PSVYSTSKDTKYQSVYV--SEKDEC-IAT 576  
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Db 661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
QY 577 EV 578  
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Db 721 EV 722  
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RESULT 9  
US-09-783-931-12  
; Sequence 12, Application US/09783931  
; Publication No. US20030073620A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/783,931  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 722 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-783-931-12

Query Match 72.8%; Score 2462; DB 10; Length 722;  
Best Local Similarity 75.9%; Pred. No. 5.2e-171;  
Matches 548; Conservative 6; Mismatches 24; Indels 144; Gaps 68;  
QY 1 MGR-----LLASALLC---VSGVFELKLQEFVNNKKGLL-NRNCRRG-----GCCTFFR 45  
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Db 1 MGRSALALAVVSALLCQVWSSGVFELKLQEFVNNKKGLLGNRNCRRGSGPPCACRTFFR 60  
QY 46 VCLKHYQASVSPEPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPGTFS 100  
|||  
Db 61 VCLKHYQASVSPEPCTYGSVTPVLGVDSFSLPDGAGIDPAFSNPIRPFPGFTWPGTFS 120  
|||  
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRLH-VGEEWSQDLHSSGRTDL-YSYRFVCD 156  
|||||

Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRLHVTGEEWSQDLHSSGRTDLRYSYRFVCD 180  
QY 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DOHG-CDKPG 209  
|||  
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGKMDPGWKQYCTDPICLPGCDDHGKCDKPG 240  
QY 210 ECKRVGWQGRYCDDECIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC-NG 268  
|||  
Db 241 ECKRVGWQGRYCDDECIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300  
QY 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK 317  
|||  
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360  
QY 318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367  
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Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCPCPLGFSGFNCEKKMDLCSGSSPCSNGAKCV 420  
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPGY-GKNCS-P 415  
|||  
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480  
QY 416 VSRCEH-PCNHGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458  
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Db 481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540  
QY 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503  
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Db 541 GPFPWAVACGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGCTETMNNLANCQREK 600  
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV-----LK 536  
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Db 601 DVSVSIIGATQIKNTNKKADFHDGHAESKSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660  
QY 537 VHKCSEKALRKR-----PSVYSTSKDTKYQSVYV--SEKDEC-IAT 576  
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Db 661 RDTKCQSLSQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720  
QY 577 EV 578  
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Db 721 EV 722  
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RESULT 10  
US-10-417-719-4  
; Sequence 4, Application US/10417719  
; Publication No. US20030180784A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: McCarthy, Sean  
; APPLICANT: Gearing, David  
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF  
; FILE REFERENCE: MBIO1997-002CP2M  
; CURRENT APPLICATION NUMBER: US/10/417,719  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US/09/568,218  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 08/872,855  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 08/832,633  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 720  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
; US-10-417-719-4

Query Match 72.5%; Score 2454; DB 14; Length 720;  
Best Local Similarity 76.4%; Pred. No. 2e-170;  
Matches 551; Conservative 6; Mismatches 20; Indels 144; Gaps 71;

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Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTPFR 45
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Db 1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR 60
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    : |||||
Qy 46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSPNPIRFPFGFTWPGTFS 100
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    : |||||
Db 61 VCLKH-QASVSPEPPCTYGSAPTAVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 119
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    : |||||
Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHLVGEESQDLHSSGRTDL-YSYRFVCDDEH 157
    |||||
    : |||||
Db 120 LIIEALHTDSPDDLATENPERLISRLTTQRHTVGEESQDLHSSGRTDLRYSYRFVCDDEH 179
    |||||
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Qy 158 YYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPGE 210
    |||||
    : |||||
Db 180 YYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKQYCTDPICLPGCDDQHGYCDKPGE 239
    |||||
    : |||||
Qy 211 CKCRVWQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGA 269
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    : |||||
Db 240 CKCRVWQGRYCDICIRYPGCLHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNA 299
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    : |||||
Qy 270 TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPPGFYGK- 317
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    : |||||
Db 300 TCTNTGQGSYTCSCRPGYTGANGCELEVDECAPSPCKNGASCTDLEDSECTCPPPGFYGKV 359
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    : |||||
Qy 318 CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CVD 368
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    : |||||
Db 360 CELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGLFSGFNCEKKMDLGGSSPCSNGAKCVD 419
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Qy 369 LGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PV 416
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    : |||||
Db 420 LGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDSECTCPPGYTGKNCSAPV 479
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    : |||||
Qy 417 SRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ-- 458
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    : |||||
Db 480 SRCEHAPCHNGATCHORQORYMCECAQGYGGPNQCQFLLPEPPPGPMVVDLSERHMESQGG 539
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Qy 459 -FPW-AVCAGLV--L-LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREKD 504
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Db 540 PFPWAVACAGVVLVLLLLGCAA-VVCVRLKQLQKHQPPPEPCGGETETMNNLANCQREKD 599
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    : |||||
Qy 505 ---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK- 540
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    : |||||
Db 600 VSVSIGATQIKNTNKKADFHGDHGAKKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSKR 659
    |||||
    : |||||
Qy 541 -----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATE 577
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    : |||||
Db 660 DTKQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIATE 719
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Qy 578 V 578
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Db 720 V 720

RESULT 11
US-10-417-719-5
; Sequence 5, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT APPLICATION NUMBER: US/10/417,719
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 08/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 08/832,633
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Rattus No. US20030180784A1vegicus
US-10-417-719-5

Query Match      72.3%; Score 2447.5; DB 14; Length 713;
Best Local Similarity 75.7%; Pred. No. 5.8e-170;
Matches 540; Conservative 9; Mismatches 29; Indels 135; Gaps 66;

Qy 1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTPFR 45
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Db 1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR 60
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    : |||||
Qy 46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSPNPIRFPFGFTWPGTFS 100
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    : |||||
Db 61 VCLKHYQASVSPEPPCTYGSAPTAVLGVDSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 120
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Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHLVGEESQDLHSSGRTDL-YSYRFVCDDEH 157
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    : |||||
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHTVGEESQDLHSSGRTDLRYSYRFVCDDEH 180
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Qy 158 YYGEGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPGE 210
    |||||
    : |||||
Db 181 YYGEGSVFCRPRDDAFGHFTCGRGEKMDPGWKQYCTDPICLPGCDDQHGYCDKPGE 240
    |||||
    : |||||
Qy 211 CKCRVWQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGA 269
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    : |||||
Db 241 CKCRVWQGRYCDICIRYPGCLHGTCCQPPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNA 300
    |||||
    : |||||
Qy 270 TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPPGFYGK- 317
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    : |||||
Db 301 TCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGGSCDTDLEDSECTCPPPGFYGKV 360
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Qy 318 CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSSPC-NGA-CVD 368
    |||||
    : |||||
Db 361 CELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKIDLCSPPSCSNGAKCVD 420
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Qy 369 LGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PV 416
    |||||
    : |||||
Db 421 LGNSYLCRCQOTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDSECTCPPGYTGKNCSAPV 480
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    : |||||
Qy 417 SRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPPGPV---DEEQFPW-AVC 464
    |||||
    : |||||
Db 481 SRCEHAPCHNGATCHORQORYMCECAQGYGGANCFLLPEPPPDLLIVAAQGGSPFWAVC 540
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Qy 465 AGLV--L-LLLLGCAA-VVCVRLK----QKP--EC--ETETMNNLANCQREKD---SSIGA 509
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Db 541 AGVVLVLLLLLGCAA-VVCVRLKQLQKHQPPPPDPCGGETETMNNLANCQREKDVSVSIIGA 600
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Qy 510 TQIKNTNKK-DFH-----DK---KVRYP-VDYNLV--LK-----VHKK----- 540
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Db 601 TQIKNTNKKADFHGDHGADKSSFKARYPTVDYNLIRDLKGDEATVRDAHSKRDTKCOSQG 660
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Qy 541 -CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
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RESULT 12
US-10-042-865-108
; Sequence 108, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
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APPLICANT: Patturajan, Meera  
APPLICANT: Vernet, Corine A.M  
APPLICANT: Taylor, Sarah  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Miller, Charles E  
APPLICANT: Guo, Xiaojia  
APPLICANT: Boldog, Ference L  
APPLICANT: Grosse, William M  
APPLICANT: Alsobrook II, John P  
APPLICANT: Gerlach, Valerie L  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Rothenberg, Mark E  
APPLICANT: Ellerman, Karen  
APPLICANT: MacDougall, John  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John  
APPLICANT: Smithson, Glennda  
APPLICANT: Gunther, Erik  
APPLICANT: Stone, David  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
TITLE OF INVENTION: Using the Same  
FILE REFERENCE: 21402-537  
CURRENT APPLICATION NUMBER: US/10/042,865  
CURRENT FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/260,417  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 60/260,831  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: 60/272,338  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: 60/274,876  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/284,704  
PRIOR FILING DATE: 2001-04-18  
NUMBER OF SEQ ID NOS: 264  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 108  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-042-865-108

Query Match 72.0%; Score 2436; DB 15; Length 714;  
Best Local Similarity 75.4%; Pred. No. 4e-169;  
Matches 538; Conservative 11; Mismatches 29; Indels 136; Gaps 66;  
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QY 46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPPTFS 100  
Db 61 VCLKHYQASVSPEPPCTYGSAVAVLGVDSFSLPDGAGIDPAFSNPIRPFPGFTWPPTFS 120  
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156  
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180  
QY 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKQYCT-PICLPGC-DQHG-CDKPG 209  
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGERGEKMCDFGWKQYCTDPICLPGCDDQHGCDKPG 240  
QY 210 ECKCRVWGQGRYDCIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268  
Db 241 ECKCRVWGQGRYDCIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300  
QY 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYK 317  
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVECAPSCRNGGSCTDLEDYSCTCPPGFYK 360  
QY 318 -CELSAMTCADGCPFCNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CV 367

Db 361 VCELSAMTCADGCPFCNGGRCSDNPDGGYTCHCPAGSFGNCEKKIDLCSSSPCSGAKCV 420  
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415  
Db 421 DLGNSYLCRCQTGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCCTCPPGYTCRNC SAP 480  
QY 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPPGPV-----DEEOPPW-AV 463  
Db 481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGANGCQFLLPEPPDLIVAAQGGSPFWAV 540  
QY 464 CAGLV--L LLLGCAA-VVCRLK---QKP--EC--ETETMNNLANCQREKD---SSIG 508  
Db 541 CAGVLLV L LLLGCAA VVCRLK LQKHQPPDPGCGETETMNNLANCQREKDVSVSIIG 600  
QY 509 ATQIKNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC--- 541  
Db 601 ATQIKNTNKKADFGHDGADKSSFKARYPTVDYNLIRDLKGDEATVRDAHSKRDTKCQSQ 660  
QY 542 ---SEEKAL-----RKRP-SVYSTSKDTKYQSVV--SEKDEC-IATEV 578  
Db 661 GSVGEKSTSTLRGGEVDPDRKRPEVSYSTSKDTKYQSVVLSAEKDECVIATEV 714  
RESULT 13  
US-09-828-366-21  
; Sequence 21, Application US/09828366  
; Patent No. US20020010137A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klein, Robert D.  
; APPLICANT: Napier, Mary  
; APPLICANT: Wood, William I.  
; APPLICANT: Yuan, Jean  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
; TITLE OF INVENTION: CELL GROWTH  
; FILE REFERENCE: P1694R1C1  
; CURRENT APPLICATION NUMBER: US/09/828,366  
; CURRENT FILING DATE: 2001-04-05  
; Prior filing data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 21  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-828-366-21

Query Match 71.0%; Score 2401.5; DB 9; Length 723;  
Best Local Similarity 75.1%; Pred. No. 1.3e-166;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;  
QY 7 SALLC---VSGVFELKLOEFVNKKGLL-NRNCRRGG-----GCCTFFRVCLKHYQASVS 56  
Db 13 SALLCQVSSGVFELKLOEFVNKKGLLGNRNCRRGGAGPPPCACRTFFRVCLKHYQASVS 72  
QY 57 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPFPGFTWPPTFSLIIEALHTDSP 111  
Db 73 PEPPCTYGSAVTPVLGVDSFSLPDGAGADSAFSNPIRPFPGFTWPPTFSLIIEALHTDSP 132  
QY 112 DDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHYHGGCSVFC 167  
Db 133 DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRTDLKYSYRFVCDHYHGGCSVFC 192  
QY 168 RPRDD-FGHFTCG-RGEK-C-PGWKQYCT-PICLPGCD-QHG-CDKPGECKCRVWGQR 220  
Db 193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWGQR 252  
QY 221 YCDECIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279  
Db 253 YCDECIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY 312





Search completed: November 29, 2004, 13:42:04  
Job time : 62.226 secs

; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/089947  
 ; PRIOR FILING DATE: 1998-06-19  
 ; PRIOR APPLICATION NUMBER: 60/090349  
 ; PRIOR FILING DATE: 1998-06-23  
 ; PRIOR APPLICATION NUMBER: 60/090429  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090445  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090538  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07

Query Match 71.0%; Score 2401.5; DB 14; Length 723;  
Best Local Similarity 75.1%; Pred. No. 1.3e-166;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy	7	SALLC-- --VSGVFELKLOEFVNKKGLL--NRNCCRGG-----GCCTFFRVCCLKHYQASVS	56
Db	13	SALLCQVWSSGVFELKLOEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVCCLKHYQASVS	72
Qy	57	PEPPCTYGSA--TPVLG--SFS--PDGAG--DPAFSNPIRFPFGFTWGTFTPSLIIEALHTDSP	111
Db	73	PEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWGTFTPSLIIEALHTDSP	132
Qy	112	DDL--TENPERLISRL--TORHL--VGEWSQDLHSSGRITDL--YSYRFVCDHYHGGCSVFC	167
Db	133	DDLATENPERLISRLATQRHLTVGEWSQDLHSSGRITDLKYSYRFVCDHYHGGCSVFC	192
Qy	168	RPRDD--FGHFTCG--RGEK--C--PGWKGOYCT--PICLPGCD--QHG--CDKPGECKCRVWQGR	220
Db	193	RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGR	252
Qy	221	YDECIRYPGCVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPC--NGATCTNTGQGSY	279
Db	253	YDECIRYPGCLHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSY	312
Qy	280	TCSCRPGYTG--CE-- --EEC-- --PCKN--GSCTDLES--SCTCPPGFGYK--CELSAMTCAD	327
Db	313	TCSCRPGYTATGATCELGIDECDPSPCKNGGSCDTLENSYSCTCPPGFGYKICELSAMTCAD	372
Qy	328	GPCFNGGRC--DNPDDGY--C--CPLG--SGFNCEKK-- --DCSSPC--NGA--CVDLGNYSY--C--CQ	376
Db	373	GPCFNGGRCSDSPDGGYSCRCPPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ	432
Qy	377	AGF--GR--C--DNVDDCA--SPC--NGGTC--DVND--SCTCPPGY--GKNCS--PVSRCHEH--PCHN	425
Db	433	AGFSGRHCDNDVDDCASSPCANGGTCTRDGVNDFSTCTPPGYTGRNCSAPVSRCEHAPCHN	492
Qy	426	GATCHRR-- --YCECA--GYGG--NCQFLLPPE--PPGP-- --VD-- --EEQ-- --FPW--AVCAGL	467
Db	493	GATCHERGHRYVCECARGYGGPNCQFLLPPELPPGPAVVDLTEXLEGGGPPFPVAVCAGV	552
Qy	468	VL-- --LLLLGCAA--VVCVRL-- --KQKPEC-- -- --ETETMNLANCOREKD-- --SSIGATQI	512
Db	553	ILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNLANCOREKDISVSIIGATQI	612
Qy	513	KNTNKK--DFH-- --DK-- --KVRYP--VDYNLV-- -- --LKVHKKC-- -- --S	542
Db	613	KNTNKKADFHGDHSDAKNGCFKARYPAVDYNLVQDLKGGDDTAVRDAHSKRDTKCQPQSGG	672
Qy	543	EKKAL-- -- -- --RKRP--SVYSTSKOTKYQSVYV-- --SEKDEC--IATEV	578
Db	673	EKGTPTTLRGGEASERKRPPDSGCSTSKOTKYQSVYVISEEKDECVIATEV	723



GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: November 29, 2004, 13:16:29 ; Search time 14.4855 Seconds  
(without alignments)  
3839.238 Million cell updates/sec

Title: US-09-783-931-13  
Perfect score: 3383  
Sequence: 1 MGRLLASALLCVSGVFELKL.....DTKYQSVVSEKDECIATEV 578  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	73.6	728	2 I50719	C-Delta-1 - chicke
2	2466	72.9	722	2 I48324	DELTA-like 1 - mou
3	1329.5	39.3	685	2 JC7570	Delta-4 protein -
4	1298.5	38.4	686	2 JC7569	Delta-4 protein -
5	1086.5	32.1	833	2 S19087	gene Delta protein
6	1085.5	32.1	832	2 A31246	neurogenic protein
7	1084.5	32.1	880	2 S00670	neurogenic repetit
8	935.5	27.7	1220	2 A56136	jagged protein pre
9	758.5	22.4	1408	2 S16148	gene serrate prote
10	496.5	14.7	2437	2 S42612	transmembrane prot
11	492.5	14.6	2524	2 A35844	Xotch protein - Af
12	491	14.5	385	2 S53718	homeotic protein d
13	489.5	14.5	2531	2 A46019	notch-1 protein -
14	485	14.3	1203	2 A49175	Motch B protein -
15	484.5	14.3	2531	2 S18188	notch protein homo
16	484	14.3	385	2 A54785	preadipocyte facto
17	478	14.1	2471	2 A49128	cell-fate determin
18	473.5	14.0	2531	2 T31070	notch homolog - se
19	464	13.7	2318	2 S45306	notch 3 protein -
20	461	13.6	383	2 S53716	delta-like homeoti
21	459	13.6	2555	2 A40043	notch protein homo
22	456.5	13.5	2352	2 T30201	Notch homolog prot
23	454	13.4	1064	2 A40136	fibropellin Ia - s
24	450	13.3	308	2 JC7125	epidermal growth f
25	448	13.2	2703	1 A24420	notch protein - fr
26	445.5	13.2	2321	2 S78549	notch3 protein - h
27	441	13.0	2139	2 A35672	crumbs protein - f
28	434	12.8	1964	2 T09059	notch4 - mouse
29	424.5	12.5	861	2 A48825	Notch homolog Motc

30	421.5	12.5	1295	2 A32901	glp1 protein precu
31	413.5	12.2	1429	2 S06434	homeotic protein 1
32	405	12.0	1620	2 T27283	hypothetical prote
33	400	11.8	1722	2 E89753	protein F11C7.4 [i
34	397.5	11.7	1574	2 T13954	MEGF6 protein - ra
35	387	11.4	473	2 A56175	adhesive plaque pr
36	386.5	11.4	2201	2 A32160	tenascin-C - human
37	378	11.2	570	2 A48836	fibropellin C prec
38	376.5	11.1	2019	1 JQ1322	tenascin precursor
39	375	11.1	1372	2 T25933	hypothetical prote
40	371	11.0	1746	1 S19694	tenascin precursor
41	367	10.8	3566	1 A40701	tenascin-X precurs
42	367	10.8	4006	2 T09070	probable tenascin
43	365	10.8	1111	2 T26972	hypothetical prote
44	352.5	10.4	1810	1 A32230	tenascin precursor
45	350	10.3	4135	2 T42629	tenascin-X - bovin

ALIGNMENTS

RESULT 1  
I50719  
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C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50719  
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.  
Nature 375, 787-790, 1995  
A;Title: Expression of a Delta homologue in prospective neurons in the chick.  
A;Reference number: I50719; MUID:95319507; PMID:7596411  
A;Accession: I50719  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-728 <HEN>  
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g8824  
C;Superfamily: delta-4 protein; EGF homology  
F;299-332/Domain: EGF homology <EGX1>  
F;339-370/Domain: EGF homology <EGF1>  
F;416-447/Domain: EGF homology <EGX2>  
F;454-485/Domain: EGF homology <EGF>  
F;492-523/Domain: EGF homology <EGF3>

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Db	71	KHYQASVSPEPCTYGSAITPVLGANSFSVPDGAGADPAFSPNPIRFPFGFTWPGTFSLI	130				
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Db	131	IEALHTDSPDDLTTENPERLISRLATQRHLAVGEWSQDLHSSGRTDLKYSVRFVCDHY	190				
QY	159	YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKQYCT-PICLPGCD-QHG-CDKPGEC	211				
Db	191	YGEGCSVFCRPRDDRFHFTCGERGEKVCNPGWKQYCTEPICLPGCDEQHGFCDKPGEC	250				
QY	212	KCRVGWQGRYCDICIRYPGCVHGTCQQPWQNCQEGWGGLFCNQDLNYCTHHKPC-NGAT	270				
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QY	271	CTNTGQSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGYGK-C	318				
Db	311	CTNTGQSYTCSCRPGYTGSSCEIEINECDANPCKNGGSGCTDLENSYCTCPPGYGKNC	370				
QY	319	ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL	369				

Db 371 ELSAMTCADGPCFNGGRCCTDNPDDGGYSCRCPLGYSGFNCCKIDYCSSSSPCANGAQCVDL 430

Qy 370 GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417

Db 431 GNSYICQCOAGFTGRHCDNDVDDCASFPVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVS 490

Qy 418 RCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLPPEP-GPV-----DEEQ 458

Db 491 RCHNPCHNGATCHERSNRYVCECARGYGGLNCQFLPPEPQGPVIVDFTEKYTEGQNSQ 550

Qy 459 FPW-AVCAGLVL---LLLGC AA-VVCVRLK-----QKPEC---ETETMNNLANCQREKD- 504

Db 551 FPWIAVCAGIILVLMLLGCAAIWVCVRLKVQKRHHQPEACRSETETMNNLANCQREKDI 610

Qy 505 --SSIGATQIKNTNKK-DFH----DK--KVRYP-VDYNLVLKV-----HKKC--- 541

Db 611 SISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPVSDYNLVHELKNEDSVKEEHGKCEAK 670

Qy 542 -----SEEKAL-----RKRP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV 578

Db 671 CETYDSEAEKSAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEKDECIATEV 728

RESULT 2

I48324

DELTA-like 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48324

R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.

Development 121, 2407-2418, 1995

A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin

A;Reference number: I48324; MUID:95401858; PMID:7671806

A;Accession: I48324

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-722 <RES>

A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065

C;Genetics:

A;Gene: Dll1

C;Superfamily: delta-4 protein; EGF homology

F;331-362/Domain: EGF homology <EGF2>

F;446-477/Domain: EGF homology <EGF>

F;484-515/Domain: EGF homology <EGF1>

Query Match 72.9%; Score 2466; DB 2; Length 722;

Best Local Similarity 76.6%; Pred. No. 2.7e-144;

Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

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Qy 46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSPNPIRFPFGFTWPGTFS 100

Db 61 VCLKHYQASVSPEPPCTYGSATPVLGVDVSFSLPDGAGIDPAFSPNPIRFPFGFTWPGTFS 120

Qy 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156

Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD 180

Qy 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209

Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKQYCTDPICLPGCDDQHGYCDKPG 240

Qy 210 ECKCRVWQGRYCYDECIRYPGCVHGTCCQOPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268

Db 241 ECKCRVWQGRYCYDECIRYPGCLHGTCCQOPWQCNCQEGWGLFCNQDLNYCTHHKPCFNG 300

Qy 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCXNG-SCTDLES--SCTCPPGFYGK 317

Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSPSCTCPPGFYGK 360

Qy 318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367

Db 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCSSSPCSNGAKCV 420

Qy 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415

Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSTCTPPGYTGKNCSAP 480

Qy 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLLPE-PPGP--VD-----EEQ- 458

Db 481 VSRCEHAPCHNGATCHORQORYMCECAQYGGPNCOFLLLPEPPGPMVVDLSERHMSQG 540

Qy 459 --FPW-AVCAGLV---LLLGC AA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503

Db 541 GPFPWAVACAGVVLVLLLLGC AA-VVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK 600

Qy 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540

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Db 661 RDTKCQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720

Qy 577 EV 578

Db 721 EV 722

RESULT 3

JC7570

Delta-4 protein - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C;Accession: JC7570

R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J.

J. Biochem. 129, 27-34, 2001

A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A;Reference number: JC7569; MUID: 21064937; PMID:11134954

A;Accession: JC7570

A;Molecule type: mRNA

A;Residues: 1-685 <YON>

A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894

C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane rec

ates the Notch signaling, the growth or differentiation of vascular endothelial cells.

C;Genetics:

A;Gene: delta-4

C;Superfamily: delta-4 protein; EGF homology

C;Keywords: transmembrane protein

Query Match 39.3%; Score 1329.5; DB 2; Length 685;

Best Local Similarity 46.4%; Pred. No. 1.6e-74;

Matches 314; Conservative 81; Mismatches 154; Indels 127; Gaps 52;

Qy 13 SGVPFELKLQEFVNKKGLL--NRNCCRGCGCCTFFRVCLKHYYQASVSPEPPCTYGS-ATPV 69

Db 27 SGVFQLQLQEFINERGVLASGRPC--EPGCRTFFRVCLKHFAQVWSP-GPCTFGTVSTPV 83

Qy 70 LG--SFS PDGAGDPAFSPNPIRFPFGFTWPGTFSLIIEALHTDSPDDL TEN---PERLISR 124

Db 84 LGTNSFAVRDDSSGGGNPLQLPFNFTWPGTFSLIIEAWHAPG-DDLRPEALPPDALISK 142

Qy 125 LT-QRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHYHGECSVFCRPRDD-FGHFTC-- 178

Db 143 IAIQGS LAVGQNWLLDEQTSTLRLRYSYRVICSDNYGDNCSRLCKKRNDFHGHYVQCP 202

Qy 179 -GRGEKCPGWKGQYC-TPICLPGC-DQHG-CDKPGECKRVGWQGRYCYDECIRYPGCVHG 234

Db 203 DGNLSCLPGWTGEYCCQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNECIPHNGCRHG 262

Qy 235 TCQQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPGYTG--CE 291

Db 263 TCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTCCTCRPGYTGVDCE 322

Qy	292	---EEC---PCKN-GSCTDLESS--CTCPPGFYG-KCELSAMTCADGCPFNGGRC--DNP	339
Db	323	LELSECDSNPCRNGGSKQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCRERNQ	382
Qy	340	DGGYCC--PLGSGFNCCK--DC-SSPC--NGACVDLGNS-YC-COAGP--GRCD-NVD	386
Db	383	GANYACECPNFTGNSCEKVKDRCTSNPCANGGQCLNRGSPRMCRCRPGFTGTYCELVHS	442
Qy	387	DCA-SPC-NGGTC-DVNDs--CTCPPGY-GKNC--SPVSR-CEHPCHNGATCHRR----	432
Db	443	DCARNPCAHHGTCHDLENGLMCTCPAGFSRRCEVRTSIDACASSPCFNATCTYDLSTD	502
Qy	433	--YCECA-GY-GGNCQFLLPEPPGPVDEEQFPW-AVCAG---LVLLLLGCAAVVC--VR	481
Db	503	TFVCNCPYGFVGSRCFPPVGLPP-----SFPWVAVSLGVGLAVLLVLLGMVAVAVRQLR	556
Qy	482	LKQKPECETETMNNLANCQREKDDSSIGATQIKNTN-KKDFH-----DKKVRYPVD	530
Db	557	LRRPDDGSREAMNNLSDFQ--KDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQONHTLD	614
Qy	531	YNLV-----LKVHKKCSEKALRKPSPVYSTSKDTKYQSV	565
Db	615	YNLAPGPLGRGTMPCGKPFHSDKSLGEKAPRLHSEKPE-----CRISAICSPRDSMYQSV	669
Qy	566	YV--SEKDEC-IATEV	578
Db	670	CLISEERNECVIATEV	685

## RESULT 4

JC7569  
Delta-4 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: JC7569  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;  
J. Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.  
A;Reference number: JC7569; MUID: 21064937; PMID:11134954  
A;Accession: JC7569  
A;Molecule type: mRNA  
A;Residues: 1-686 <YON>  
A;Cross-references: UNIPROT:Q9DBU9; DDBJ:AB043893  
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re  
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.  
C;Genetics:  
A;Gene: delta-4  
C;Superfamily: delta-4 protein; EGF homology

Query Match	38.4%;	Score 1298.5;	DB 2;	Length 686;
Best Local Similarity	45.7%;	Pred. No. 1.3e-72;		
Matches 311;	Conservative 80;	Mismatches 153;	Indels 137;	Gaps 51;
QY	13	SGVFELKLOEFVNKKGLL-NRNCRCGGGCTFFRVCLKHYYQASVSPEPPCTYGS-ATPVL	70	
Db	28	SGIFQLRLQEFVNQRMGLANGQSCE-PGCRTRFFRICLKHFAQTFS-EGPCTFGNVSTPVL	85	
QY	71	GSFS-----PDGAGDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDL---TENPERL	121	
Db	86	GTNSFVVRDKNSGSG---RNPLQLPFNFTWPGTFSLNIQAWHTPG-DDLRPETSFGNSL	140	
QY	122	ISR-LTORHL-VGEEWSQDLHSSGRTDL-YSYRFVCDHHYYGEGSCSVFCRPRDD-FGHFT	177	
Db	141	ISQIIIGSLAVGKIWRTEQNDTLTRLSSYSYRVICSDNYYGESCSRLCKKRRDHFHGYE	200	
QY	178	C---GRGEXCPGWKGQYC-TPICLPGC-DQHG-CDKPGECKRVGWQGRYCDECIYPGC	231	
Db	201	CQPDGSLCLPGWTGKYCDQPICLSGCHEQNGYCSKPDEICIRPGWQGRLCNECIPHNCG	260	
QY	232	VHGTCCQPMQNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPGYTG-	289	
Db	261	RHGTCISIPWQACDEGWGGLFCDQDLNYCTHSPCKNGSTCSNSGPKGYTCTCLPGYTGE	320	

Qy	290	-CE---EEC--PCKN-GSCTDLESS--CTCPPGFYGK-CELSAMTCADGPCFNGGRC--	336
Dd	321	HCELGLSKCASNP CRNGGSKDQENSYHCLCPPGYGQHCEHSTLT CADSPCFNGGSCRE	380
Qy	337	DNPDDGGYCC--PLGSGFNCEKK--DC-SSPC--NGACVDLGN SYCCQA--GF--GRCD-	383
Dd	381	RNOGSSYACECPPNFTGSNCEKKVDRCTSNPCANGGCQNRP SRTCRCRPGFTGT HCEL	440
Qy	384	NVDDCA-SPC-NGGTC-DVNDS--CTCPPGY-GKNCSPVSRCEH-----PCHNGATCH-	430
Dd	441	HISDCARSPCAHGTC HDLENGPVCTCPAGFSRRCE--VRITHDACASGPCFN GATCYT	498
Qy	431	-----RRYCECA-GY-GGNCQFLLP EPPGPVDEEQFPW-AVCAG-----LVLLLLLGCAA	476
Dd	499	GLSPNNFCVNCPIYGVGSRCEFFVG LPP-----SFPWVA VSLGVLVLLVLLVMVVVA	552
Qy	477	VVCVRLKQKPECETETMTNNLANCQREKDSSIGATQIKNTN-KKDFH-----DKKV	525
Dd	553	VRQLRLRRPDDESREAMNNLSDFQ--KDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKLQ	610
Qy	526	RYPVDYNLV-----LKVHKKCSEEKALRKRP SVYSTSKDT	560
Dd	611	NHTLDYNLAPGLLRGGM PGKYPHSDKS LGCEKVPLRLHSEKPE-----CRISAICSPRDS	665
Qy	561	KYQSIVVY--SEKDEC-IATEV	578
Dd	666	MYQSVCLISEERNECVIATEV	686

## RESULT 5

S19087  
gene Delta protein precursor - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S19087  
R;Muskavitch, M.A.T.  
submitted to the EMBL Data Library, June 1991  
A;Reference number: S19087  
A;Accession: S19087  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-833 <MUS>  
A;Cross-references: UNIPROT:P10041; EMBL:Y00222  
C;Genetics:  
A;Gene: FlyBase:D1  
A;Cross-references: FlyBase:FBgn0000463  
C;Superfamily: neurogenic protein delta; EGF homology  
F;335-371/Domain: EGF homology <EGF1>  
F;378-415/Domain: EGF homology <EGX1>  
F;457-488/Domain: EGF homology <EGF>  
F;533-564/Domain: EGF homology <EGF3>  
  
Query Match 32.1%; Score 1086.5; DB 2; Length 833;  
Best Local Similarity 38.1%; Pred. No. 1.6e-59;  
Matches 252; Conservative 67; Mismatches 177; Indels 165; Gaps 40;









F;283-316/Domain: EGF homology <EG01>		F;319-348/Domain: EGF homology <EG02>		F;355-388/Domain: EGF homology <EG03>		F;395-488/Domain: EGF homology #status atypical <EG04>		F;495-526/Domain: EGF homology <EG05>		F;533-608/Domain: EGF homology #status atypical <EG06>		F;615-645/Domain: EGF homology <EG07>		F;652-683/Domain: EGF homology <EG08>		F;690-720/Domain: EGF homology <EG09>		F;727-796/Domain: EGF homology #status atypical <EG10>		F;803-834/Domain: EGF homology <EG11>		F;841-876/Domain: EGF homology <EG12>		F;883-914/Domain: EGF homology <EG13>		F;921-952/Domain: EGF homology <EG14>		F;997-1060/Region: cysteine-rich		F;1222-1246/Domain: transmembrane #status predicted <TM1>		F;1247-1408/Domain: intracellular #status predicted <INT>		F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn	
Query Match		22.4%;		Score 758.5;		DB 2;		Length 1408;		Best Local Similarity		31.5%;		Pred. No. 3.4e-39;		Matches 211;		Conservative 63;		Mismatches 150;		Indels 245;		Gaps 43;											
Qy	10	LCVSGVFELKQEFVNKKG-LLNRNCC-----RGGGCCTFFRVCLKHQO----	52																																
Db	81	ISAAGNFELEILEISNTNSHLNGYCCGMPAELRATKTIQCSPTTAFRLCLKEYQTTEQ	140																																
Qy	53	-ASVSPEPPCTYGSA-TPVLGS---FSPDGAGDPAFNSPIRPFPGFTWPGTFSLIIEAL	106																																
Db	141	GASIS--TGCSFGNATTKILGSSFVLSDPGVG-----AIVLPFTFRWTKSFTLILQAL	192																																
Qy	107	---HTDSPDDLTENPERLISRLTQRHLV--GEEWSQDLHSSGRDLYSY--RFVCDDEHYV	159																																
Db	193	DMNTSYPD-----AERLIEETSYSGVILPSPPEW-KTLDHIGRNARITYRVRVQCAVYY	246																																
Qy	160	GEGSVFCRPRDD-FGHFTCG-RGEK--CPGWKGOYC-TPICLPGCDQ-HG-CDXPGECK	212																																
Db	247	NTTCTTFCRPRDDQFGHYACSGEGQKCLNGWQGVNCEBAICKAGCDPVHGKCDRPGECE	306																																
Qy	213	CRVGWQGRYCDECIRYPGCVHGTQO-QPWQNCQEGWGGLFCNQDLNYCTHHKPC-NGAT	270																																
Db	307	CRPGWRGPLCNECMVYPGCKHSGCSAWKVCVDTNWGGILCDQDLNFCGTHEPCKHGGT	366																																
Qy	271	CTNTGQGSYTCSCRPGYTGCEEC-----PCKNGSCTDLESS-----	307																																
Db	367	CENTAPDKYRCTCAEGLSG--EQCEIVEHPCATRPCRNGGTCTLKTNSRRTQAVYRTSHG	424																																
Qy	308	-----	315																																
Db	425	RSNMGRPVRRSSSMRSLDHLRPEQALNGSSSSGLVSLGSLQQLAPDFTCDCAAGWT	484																																
Qy	316	G-KCELSAMTCADGPCFNGGRCNDPDGGY-C-CP-----	346																																
Db	485	GPTCEINIDECAGGPCEHGGTCTIDLIGGFRCECPPEWHGDCVQVDVNECEAPHSAGIAAN	544																																
Qy	347	-----LGS-----	349																																
Db	545	ALLTTTATAIIGSNLSSALLAALTSAAVASTSLAIGPCINAKECRNQPGSFACICKEGWG	604																																
Qy	350	GFMCEKK--DCSSPC-NGA-CVDLGNYSY--CCQAGF-GR-CD-NVDDCA-SPC-NGGTC-	397																																
Db	605	GVTCAENLDDCVGQCRNGATCIDLVDNYRCACASGFTGRDCETDIDECATSPCRNGGECV	664																																
Qy	398	DV--NDSCTCPGGY-----KNCSPVSRCEHPCHNGNATCHRRYCECA--GYGGNCQF	445																																
Db	665	DMVGKFNICPLGYSGSLCEEAKENCTPSPCLEGHCLN--TPEGYCHCPPDRAGHCEQ	722																																
Qy	446	LLP---Epp	451																																
Db	723	LRPLCSQPP	731																																

S42612		transmembrane protein precursor - zebra fish		C;Species: Brachydanio rerio (zebra fish)		C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004		C;Accession: S42612		R;Bierkamp, C.; Campos-Ortega, J.A.		Mech. Dev. 43, 87-100, 1993		A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of		A;Reference number: S42612; MUID:94128602; PMID:8297791		A;Accession: S42612		A;Status: preliminary		A;Molecule type: mRNA		A;Residues: 1-2437 <BI>		A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g43386		C;Superfamily: notch protein; ankyrin repeat homology; EGF homology		F;755-786/Domain: EGF homology <EGF1>		F;1023-1054/Domain: EGF homology <EGF2>		F;1185-1216/Domain: EGF homology <EGF3>		F;1915-1947/Domain: ankyrin repeat homology <AN1>		F;1948-1980/Domain: ankyrin repeat homology <AN2>		F;1982-2014/Domain: ankyrin repeat homology <AN3>		F;2015-2047/Domain: an
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Db 792 E-----CASNPCL---NQSCIDDVAGFKCNC 815

RESULT 11

A35844

Xotch protein - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 16-Aug-2004

C;Accession: A35844

R;Coffman, C.; Harris, W.; Kintner, C.

Science 249, 1438-1441, 1990

A;Title: Xotch, the Xenopus homolog of Drosophila notch.

A;Reference number: A35844; MUID:90385285; PMID:2402639

A;Accession: A35844

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1-2524 <COF>

C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C;Keywords: transmembrane protein

F;146-177/Domain: EGF homology <EGX1>

F;184-215/Domain: EGF homology <EGF1>

F;222-254/Domain: EGF homology <EGF>

F;456-487/Domain: EGF homology <EGX2>

F;757-788/Domain: EGF homology <EGF3>

F;1025-1056/Domain: EGF homology <EGX3>

F;1924-1956/Domain: ankyrin repeat homology <AN1>

F;1957-1989/Domain: ankyrin repeat homology <AN2>

F;1991-2023/Domain: ankyrin repeat homology <AN3>

F;2024-2056/Domain: ankyrin repeat homology <AN4>

F;2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 14.6%; Score 492.5; DB 2; Length 2524;

Best Local Similarity 28.4%; Pred. No. 1.2e-22;

Matches 182; Conservative 61; Mismatches 190; Indels 208; Gaps 47;

QY 10 LCVSGVFELKLQEFVNKKLLNRNCCRGGGC-----CTFFRVCLKHYYQASVSPEP 59

Db 322 VCVNGWTGEDCSE--NIDDCANAAACHSGATCHDRVASFYCECPHGRTGLLCHLDNACISN 379

QY 60 PCTYGS---ATPVLGS---FSPDGAGDPAFNSPIRPFPGFTWPGTFTSLIIEALHTDSPDD 113

Db 380 PCNEGSNCDTNPNVNGKAICTCPPGYTGACNNDV-----DECS 417

QY 114 LTENPERLISRLTORHLVGEWSQDLHSSGRTDLYSRFVFCDEHYHGGGSV-----FCR 168

Db 418 LGANPCERGGRCT-----NTLGSFQCNCPOGYAGPRCEIDVNECLSN 459

QY 169 P-----RDDFGHFTCGRGEKC-PGWKGQYC-TPI-----CLPGCDQHGD 206

Db 460 PCQNDSTCLDQIGEFQC----ICMPGYEGLYCTNIDECASNPLHNGKCIDKINEFRCD 515

QY 207 KPG-----ECKCRVGMQGRYCD----ECIRYPG 230

Db 516 CPTGFSGNLCQHDDECTSTPCKNGAKCLDGPNSYTCQCTEGTGRHCEQDINECIPDP- 574

QY 231 CVHGTCCQ---PWQNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPG 286

Db 575 CHYGTCKDGIATFTCLCRPGYTGRLCDNDINECL-SKPCLNGGQCTDRENG-YICTCPKG 632

QY 287 YTG--CE---EECP---CKNGSCTDLES--SCTCPPPGFYGK-CELSAMTCADGPCFNNGR 335

Db 633 TTGVNCETKIDDCASNLCNDNGKCIDKIDGYECTCEPGYTGKLCNININECDNPNCRNGGT 692

QY 336 CDNPDGGYCCPLGSGFN-----CEKKDC-SSPC-NGACVDLGNYSY-C-COAGF--GRCD- 383

Db 693 CKDQINGFTCVCPDGYHDHMLSEVNECNSNPCTHGAACHDGVNGYKDCDEAGWSGNSCDI 752

QY 384 NVDDCAS-PC-NGGTC-DVNDS--CTCPPGY-GKNC-SPVSRC-EHPCHNGATCHRRRYCE 435

Db 753 NNNECESNPCHMNGGTCKDMTGAYICTCKAGFSGPNCQTNINECSSNPCLNHGTC---IDD 809

QY 436 CAGYGGNCQFLLPBPPGPVDEEQFPWAVCAGLVLLLLGCAAVVCV---RLKQKPECETET 492

Db 810 VAGYKCNC--MLP-----YTGAICEA---VLAPCAGSPCKNGGRCKESEDFETFS 854

QY 493 -----MNNLAN--CQREKDSISIGATQIKNTN 516

Db 855 CECPPGWQGTCEIDMNECVNRPCRN-----GAT-CQNTN 888

RESULT 12

S53718

homeotic protein dlk - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C;Accession: S53718

R;Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.

Biochim. Biophys. Acta 1261, 223-232, 1995

A;Title: dlk, pG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like sup

A;Reference number: S53716; MUID:95226449; PMID:7711066

A;Accession: S53718

A;Molecule type: mRNA

A;Residues: 1-385 <LEE>

A;Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:G562107; PIDN:AAB60495.1; PID:G5621.

C;Superfamily: preadipocyte factor 1; EGF homology

C;Keywords: transmembrane protein

F;54-85/Domain: EGF homology <EGF1>

F;92-124/Domain: EGF homology <EGF>

F;131-167/Domain: EGF homology <EGF3>

F;214-246/Domain: EGF homology <EGX1>

F;303-332/Domain: transmembrane #status predicted <TM1>

Query Match 14.5%; Score 491; DB 2; Length 385;

Best Local Similarity 32.8%; Pred. No. 3.2e-23;

Matches 126; Conservative 39; Mismatches 95; Indels 124; Gaps 23;

QY 173 FGHFTCGRGEKCPGWKGQYCTPICLPGCD-QHG-CDKPGECKRVGWQGRYCDDECIRYPG 230

Db 17 FGHSTYGAE-----CDPPCDPQYGFCEADNVCRCHVWEGPLCDKCVTAPG 62

QY 231 CVHGTCCQWPQCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSYTCSCRPGYTG- 289

Db 63 CVNGVCKEPWQCICKDGDGDKFCEIDVRACTSTPCANNGTCTVDLEKGYECSCCTPGFSGK 122

QY 290 -CEEEC-----PCKN-GSCTDLE-----SSCTCPPPGFYGK-CELSAMT--CADGPCF 331

Db 123 DCQHKAGPCVINGSPCQHGGACVDDDEQAASHASCLCPPGFSGNFCEIVAATNSCTPNPCE 182

QY 332 NGGRCDNPDGGYCCPLGSGFNCEKKDCSSPCNGACVDLGNYSYCCQAGRGCDNVDDCAS- 390

Db 183 NDGVCTDIGDFFRCRCPAGF--VDKTCRSP-----VSNCASG 217

QY 391 PC-NGGTC----DVNDSCTC-PPGYGKNC-----SPVSRCEHPCHNGATCHRRRYCECAG 438

Db 218 PCQNGGTCLQHTQVSFECLCKPPFMGPTCAKRGASPVQVTHLP-----SG 263

QY 439 YGGNCQFLPPEPPG----PVDE-EQF-----PWAVCAGLV-----LL 470

Db 264 YGLTYRL-----TPGVHELPPVQQPEQHILKVMKELNKSTPLLTEGQAICFTILGVLTSLV 319

QY 471 LLGCAAVVCVRLKQKPECETETMN 494

Db 320 VLGTVAIVFLN-----KCETWVSN 338

RESULT 13

A46019

notch-1 protein - mouse

N;Alternate names: notch protein

C;Species: Mus musculus (house mouse)

C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004

C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109

R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid

Genomics 15, 259-264, 1993

A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of







C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
F;143-174/Domain: EGF homology <EGX1>  
F;482-513/Domain: EGF homology <EGF1>  
F;560-591/Domain: EGF homology <EGF>  
F;674-705/Domain: EGF homology <EGX2>  
F;712-743/Domain: EGF homology <EGF3>  
F;836-867/Domain: EGF homology <EGX3>

Query Match 14.3%; Score 485; DB 2; Length 1203;  
Best Local Similarity 25.2%; Pred. No. 1.9e-22;  
Matches 184; Conservative 59; Mismatches 178; Indels 310; Gaps 48;

QY 34 CCRGGCCCTFFRVCLKHYQASVSP-----EPPCTYGSATPVLGSF----S 74  
Db 299 CLNDGRCIDL----VNGYQCQCPGTSGLNCEINFDDCASNPCMHGVCVDGINRYSCVCS 354  
  
QY 75 PDGAG-----DPAFSNPPIR-----FPFGFTWPGTFSLIIEALHTDSPD 112  
Db 355 PGFTGQRCNIDIDECASNPCRKGCATCINDVNGFRFCICPEGPHHPSCYSQVNECL----- 408  
  
QY 113 DLTENPERLISRLTORHLVGEWSQDLHSSGRDLYSRFVVCDEHYHGGCSV-----FC 167  
Db 409 ---SNP-----CIHGNCCTGGLSGYKCLCDAGWVGVNCEVDKNECLS 446  
  
QY 168 RPRDDFGHFTCG---RGEKC---PGWKGOYC-----TPIC 196  
Db 447 NPCQNGG--TCNNLVNGYRCTCKKGFKGYNQVNIDECASNPCLNQGTCTFDDVSGYTCHC 504  
  
QY 197 -----LPGCDQHGDCKPGECK-----CRVGWQGRYC---DECIRYP 229  
Db 505 MLPYTGKNCQTVLAPCSNPFCENAAVCKEAPNFESFSLCLAPGWQGRCTVDVDECISKP 564  
  
QY 230 GCVHGTG---QQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCR 285  
Db 565 CMNNGVCHNTQGSYVCECPGFGSGMDCEEDINDCLAN-PCQNGGSCVD-HVNTFSCQCHP 622  
  
QY 286 GYTG--CE---BEC---PCKN-GSCTDLESS--CTCPPGFYG-KCELSAMTADGPCFNG 333  
Db 623 GFIGDKCQTDMECLSEPCKNGGTCSYVNSYTCPTCPAGFHGVHCENNIDECTESSCFNG 682  
  
QY 334 GRG-----DNP--DGGYC-----CPLG-SGFN 352  
Db 683 GTCVDGINSFSLCPVGFTGPFLHDINECSSNPCLNAGTCVDGLGTYRCICPLGYTGKN 742  
  
QY 353 CEK--KDCS-SPC-----D----- 362  
Db 743 CQTLVNLCSRSPCKNKGTCVQEKARPHCLCPPGWDGAYCDVLNVSKAAALQKGVVPEHL 802  
  
QY 363 ---NGACVDLGNISYCCQAGFG----RC-DNVDDCAS-PC-NGGTCDVND-----SCTCPP 407  
Db 803 CQHSIGICINAGNTHHCQPLGYTGSYCEEQLDECASNPCQHGATC--NDFIGGYRCECVP 860  
  
QY 408 GY-GKNCS-PVSRCEH-PCHNGATC----HRRYCECAGYGGNCQFLLPEPPGP----- 453  
Db 861 GYQGVNCEYEVDECONQPCQNGGTCTIDLNVNHFKCS-----PPGTRGLLCEB 907  
  
QY 454 -VDEEQFPWAVCAGLVLLLLGCAV-----VCVRLKQKPECETETMNNLAN-CQREK 503  
Db 908 NIDE-----CAGGPHCLNGGQCVDRIIGYTCRCPLPGFAGERCEGDINECLSNPCSS- 959  
  
QY 504 DSSIGATQIKN 514  
Db 960 -GSLDCVQLKN 969

RESULT 15  
S18188  
notch protein homolog - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C;Accession: S18188  
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.  
Development 113, 199-205, 1991

A;Title: A homolog of Drosophila Notch expressed during mammalian development.  
A;Reference number: S18188; MUID:92111383; PMID:1764995  
A;Accession: S18188  
A;Molecule type: mRNA  
A;Residues: 1-2531 <WEI>  
A;Cross-references: EMBL:X57405; NID:G57634; PID:G57635  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F;987-1018/Domain: EGF homology <EGF1>  
F;1025-1056/Domain: EGF homology <EGF>  
F;1233-1264/Domain: EGF homology <EGF2>  
F;1917-1949/Domain: ankyrin repeat homology <AN1>  
F;1950-1982/Domain: ankyrin repeat homology <AN2>  
F;1984-2016/Domain: ankyrin repeat homology <AN3>  
F;2017-2049/Domain: ankyrin repeat homology <AN4>  
F;2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 14.3%; Score 484.5; DB 2; Length 2531;  
Best Local Similarity 27.5%; Pred. No. 3.7e-22;  
Matches 189; Conservative 52; Mismatches 208; Indels 239; Gaps 47;

QY 11 CVSGVFELKLOEFVNK--KGLLRNC-----CRGGGC-----TFFRVCLKHYQ 52  
Db 505 CVD-----KINEFLCQCPKGFSGHLCQYDVDECASTPCKGAKCLDGPNTYTCVCTEGYT 559  
  
QY 53 AS-----VSPEPPCTYGSATPVLGSFS---PDGAG-----DPAFSNPPIRPFPGF 93  
Db 560 GTHCEVDIDECDPD-PCHIGLCKDGVATFTCLCQPGYTGHHCTNINECHSQPCRHHGTC 618  
  
QY 94 TWPGTFSLIIEALHTDSP-----DDLTENPERLISRLTORHLVGEWSQDLHSSGR--T 145  
Db 619 QDRDNYLLCLCLKGTTGPNCEINLDDCASNP-----CDSGTCLD 657  
  
QY 146 DLYSYRFVCDHYHGGCSV-----FCRPRDDFGHFTCG----- 179  
Db 658 KIDGYECACEPGYTGSMCNVNIDECAGSPCHNGGTC--EDGIAGFTCRCPBGYHDPDTCLS 715  
  
QY 180 -----RGEKC---PGWKGOYCTPICLPQCDQHGDCKPGECK----- 212  
Db 716 EVNECNSNPCHGACRDGLNGYKCDCAPOGSGTNC-DINNNECESNPVNGGTCKDMTSG 774  
  
QY 213 ----CRVGWQGRYC---DECIRYPGCVHGTG----- 236  
Db 775 YVCTCREGFSGPNQTNINECASNPCLNQGTCTDIDVAGYKNCPLPYTGATCEWVLAPCA 834  
  
QY 237 -----QQPWQCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYT 280  
Db 835 TSPCKNSGVCKESEDYEFSCVCPTGWQGTCEIDINECV-KSPCRHAGSCQNT-NGSYR 892  
  
QY 281 CSCRPGYTG--CE---BEC---PCKN-GSCTDLESS--CTCPPGFYGK-CELSAMTCADG 328  
Db 893 CLCQAGYTGRCNESDIDDCRPNPCHNGSGSCTDGVNAAFCDCLPGFQGAFCCEEDINECATN 952  
  
QY 329 PCFNGGRCDNPDGGYCCPLGSGFN---CEKK--DCS-SPC--NGACVDLGNISY--CCQAG 378  
Db 953 PCQGANCTDCVDSYTCCTCPTGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPG 1012  
  
QY 379 F--GRCD-NVDDCAS-PC-NGGTCDVNDS-----CTCPPGY-GKNCSPVSR-CEH-PCHN 425  
Db 1013 FTGSYCYQDVNECDSPCLHGGTC--QDSYGYTKCTCPQGYTGLNQNQLVRWCDSPACKN 1070  
  
QY 426 GATCHRR-----YCEC-AGYGG-NCQFLLPEPPGPVDEEQFPWAVCA---GLVLLLLGCAA 476  
Db 1071 GKWCWQNTNTQYHCECRSGWTGFNCVDL-----SVSCEVAAQKRIGDVTLLCQHG 1119  
  
QY 477 VVCVRLKQKPECETETMNNLANCQREKD 504  
Db 1120 GLCVDDEEDKHCHCQAGYTGSYCEDEVD 1147

Search completed: November 29, 2004, 13:27:05  
Job time : 17.4855 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 29, 2004, 13:12:09 ; Search time 69.5872 Seconds  
(without alignments)  
4779.132 Million cell updates/sec

Title: US-09-783-931-13  
Perfect score: 3383  
Sequence: 1 MGRLLASALLCVSGVFELKL.....DTKYQSVYVSEKDECIATEV 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2489	73.6	728	2	Q90656	Q90656 Gallus gall
2	2466	72.9	722	1	DLL1_MOUSE	Q61483 mus musculu
3	2466	72.9	722	2	Q6PFV7	Q6pfv7 mus musculu
4	2466	72.9	722	2	AAH57400	Aah57400 mus muscu
5	2466	72.9	722	2	AAR30869	Aar30869 mus muscu
6	2466	72.9	722	2	AAH65063	Aah65063 mus muscu
7	2436	72.0	714	1	DLL1_RAT	P97677 rattus norv
8	2401.5	71.0	723	1	DLL1_HUMAN	O00548 homo sapien
9	2267.5	67.0	726	2	Q8AW87	Q8aw87 cynops pyrr
10	2262.5	66.9	721	2	Q91902	Q91902 xenopus lae
11	2084.5	61.6	720	2	Q8UWJ4	Q8uwj4 brachydanio
12	2081.5	61.5	717	2	P87357	P87357 brachydanio
13	2014	59.5	772	2	Q6DI48	Q6di48 brachydanio
14	1989.5	58.8	802	2	O57462	O57462 brachydanio
15	1383	40.9	642	2	Q7ZXT4	Q7zxt4 xenopus lae
16	1377	40.7	642	2	P79941	P79941 xenopus lae
17	1349	39.9	664	2	Q9IAT6	Q9iat6 brachydanio
18	1338.5	39.6	615	2	O57409	O57409 brachydanio
19	1329.5	39.3	685	1	DLL4_HUMAN	Q9nr61 homo sapien
20	1301.5	38.5	686	1	DLL4_MOUSE	Q9ji71 mus musculu
21	1298.5	38.4	686	2	Q9DBU9	Q9dbu9 mus musculu
22	1197.5	35.4	684	2	Q8I498	Q8i498 cupiennius
23	1086.5	32.1	833	1	DL_DROME	P10041 drosophila
24	1086.5	32.1	833	2	Q6T4M9	Q6t4m9 drosophila
25	1086.5	32.1	833	2	Q6T4N0	Q6t4n0 drosophila
26	1086.5	32.1	833	2	Q6T4N1	Q6t4n1 drosophila
27	1086.5	32.1	833	2	Q6T4N2	Q6t4n2 drosophila
28	1086.5	32.1	833	2	Q6T4N3	Q6t4n3 drosophila
29	1086.5	32.1	833	2	Q6T4N4	Q6t4n4 drosophila
30	1086.5	32.1	833	2	Q6T4N6	Q6t4n6 drosophila
31	1086.5	32.1	833	2	AAO25024	Aao25024 drosophil

32	1086.5	32.1	833	2	AAR21453	Aar21453 drosophil
33	1086.5	32.1	833	2	AAR21454	Aar21454 drosophil
34	1086.5	32.1	833	2	AAR21455	Aar21455 drosophil
35	1086.5	32.1	833	2	AAR21456	Aar21456 drosophil
36	1086.5	32.1	833	2	AAR21457	Aar21457 drosophil
37	1086.5	32.1	833	2	AAR21458	Aar21458 drosophil
38	1086.5	32.1	833	2	AAR21459	Aar21459 drosophil
39	1086.5	32.1	833	2	AAR21460	Aar21460 drosophil
40	1086.5	32.1	833	2	AAR21461	Aar21461 drosophil
41	1086.5	32.1	833	2	AAR21462	Aar21462 drosophil
42	1086.5	32.1	833	2	AAR21463	Aar21463 drosophil
43	1086.5	32.1	833	2	AAR21464	Aar21464 drosophil
44	1086.5	32.1	833	2	AAR21465	Aar21465 drosophil
45	1086.5	32.1	833	2	AAR21466	Aar21466 drosophil

ALIGNMENTS

RESULT 1  
Q90656 ID Q90656 PRELIMINARY; PRT; 728 AA.  
AC Q90656;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE C-Delta-1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spinal cord;  
RX MEDLINE=95319507; PubMed=7596411;  
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;  
RT "Expression of a Delta homologue in prospective neurons in the chick.";  
RL Nature 375:787-790(1995).  
DR EMBL; U26590; AAC59689.1; -.  
DR PIR; I50719; I50719.  
DR HSSP; P00740; LEDM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000152; AaX\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFLOOD.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW EGF-like domain.  
SQ SEQUENCE 728 AA; 79861 MW; 93B2D6666D2388B7 CRC64;

Query Match 73.6%; Score 2489; DB 2; Length 728;  
Best Local Similarity 76.0%; Pred. No. 7.3e-174;  
Matches 546; Conservative 9; Mismatches 19; Indels 144; Gaps 65;

QY 5 LASALLC-----VSGVFELKLQEFVNKGLL-NRNCRRGGG-----CCTFFRVCL 48  
DB 11 LLSALLCRCQVDSGVFELKLQEFVNKGLLSNRNCRRGGGPGGAGQQQCDCKTFFRVCL 70





FT	DISULFID	331	342	By similarity.
FT	DISULFID	336	351	By similarity.
FT	DISULFID	353	362	By similarity.
FT	DISULFID	369	380	By similarity.
FT	DISULFID	374	390	By similarity.
FT	DISULFID	392	401	By similarity.
FT	DISULFID	408	419	By similarity.
FT	DISULFID	413	428	By similarity.
FT	DISULFID	430	439	By similarity.
FT	DISULFID	446	466	By similarity.
FT	DISULFID	468	477	By similarity.
FT	DISULFID	484	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	515	By similarity.
FT	CARBOHYD	476	476	N-linked (GlcNAc...) (potential).
SQ	SEQUENCE	722 AA;	78448 MW;	95F581B56DCEC9B0 CRC64;
Query Match				
Best Local Similarity 72.9%; Score 2466; DB 1; Length 722;				
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;				
QY	1	MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTFFR	45	
Db	1	MGRRSALALAVVSALLCQVSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR	60	
QY	46	VCLKHYQASVSPEPPCTYCSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGTWPGTFS	100	
Db	61	VCLKHYQASVSPEPPCTYCSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGTWPGTFS	120	
QY	101	LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-VSYRPFVCD	156	
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRSYRPFVCD	180	
QY	157	HYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGYCT-PICLPGC-DQHG-CDKPG	209	
Db	181	HYGEGCSVFCRPRDDAFGHFTCGDRGEKMDPGWKGYCTDPICLPGCDDQHGCDKPG	240	
QY	210	ECKRVGWQGRYDCIRYPGCVHGTCCQPPWQCNQCBGWGLFCNQDLNYCTHHKPC-NG	268	
Db	241	ECKRVGWQGRYDCIRYPGCLHGTCCQPPWQCNQCBGWGLFCNQDLNYCTHHKPCRN	300	
QY	269	ATCTNTGQSYTCSRCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFGYK	317	
Db	301	ATCTNTGQSYTCSRCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSEFSCTCPPGFGYK	360	
QY	318	-CELSAMTCADGPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKDD--C-SSPC-NGA-CV	367	
Db	361	VCELSAMTCADGPCFNGRCSDNPDGGYTCHCLPFGSGFNCEKMDLCGSSPCSNCAKCV	420	
QY	368	DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P	415	
Db	421	DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGTGKNCSAP	480	
QY	416	VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ-	458	
Db	481	VSRCEHAPCHNGATCHQRGQRYMCECAQGYGPNQFLLPEPPPMPVVDLSERHMESQG	540	
QY	459	--FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK---PE-C--ETETMNNLANCQREK	503	
Db	541	GPFPWAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGGETETMNNLANCQREK	600	
QY	504	D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK	540	
Db	601	DVSVSIIGATQIKNTNKKADFGHDGAKKSSFKVRYPTVDYNLVRLDKGDEATVRDTHSK	660	
QY	541	-----CSEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT	576	
Db	661	RDTCQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT	720	
QY	577	EV	578	
Db	721	EV	722	

RESULT 3				
Q6PFV7				
ID	Q6PFV7	PRELIMINARY;	PRT;	722 AA.
AC	Q6PFV7;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	01-OCT-2004	(TREMBLrel. 28, Last annotation update)		
DE	Delta-like 1.			
GN	Name=D111;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]_TaxID=10090;			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Mouse;			
RX	MEDLINE=2238257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Mouse;			
RA	Strausberg R.;			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Mouse;			
RA	Strausberg R.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J;			
RA	Nagaraja R., Waeltz P., Brathwaite M.E.;			
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.			
CC	-I- SIMILARITY: Contains 8 EGF-like domains.			
DR	EMBL; BC057400; AAH57400.1; --			
DR	EMBL; BC065063; AAH65063.1; --			
DR	EMBL; AY497019; AAR30869.1; --			
DR	GO; GO:0005515; F:protein binding; IPI.			
DR	GO; GO:0007386; P:compartment specification; IMP.			
DR	GO; GO:0007368; P:determination of left/right symmetry; IMP.			
DR	GO; GO:0001757; P:somite specification; IMP.			
DR	InterPro; IPR000152; Asx_hydroxyl_S.			
DR	InterPro; IPR001774; DSL.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR001438; EGF_II.			
DR	InterPro; IPR006209; EGF_like.			
DR	InterPro; IPR006210; IEGF.			

DR	Pfam; PF01414; DSL; 1.	AAH57400	PRELIMINARY;	PRT;	722 AA.
DR	Pfam; PF00008; EGF; 6.	AC	AAH57400;		
DR	Pfam; PF07645; EGF_CA; 1.	DT	02-MAR-2004 (Tremblrel. 27, Created)		
DR	PRINTS; PR00010; EGFBL00D.	DT	02-MAR-2004 (Tremblrel. 27, Last sequence update)		
DR	SMART; SM00051; DSL; 1.	DT	02-MAR-2004 (Tremblrel. 27, Last annotation update)		
DR	SMART; SM00181; EGF; 8.	DE	Delta-like 1.		
DR	SMART; SM00179; EGF_CA; 6.	OS	Mus musculus (Mouse).		
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DR	PROSITE; PS00022; EGF_1; 8.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
DR	PROSITE; PS01186; EGF_2; 8.	OX	NCBI_TaxID=10090;		
DR	PROSITE; PS50026; EGF_3; 6.	RN	[1]		
DR	PROSITE; PS01187; EGF_CA; 2.	RP	SEQUENCE FROM N.A.		
KW	EGF-like domain.	RC	STRAIN=C57BL/6; TISSUE=Mouse;		
SQ	SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;	RX	MEDLINE=2238257; PubMed=12477932;		
Query Match 72.9%; Score 2466; DB 2; Length 722;					
Best Local Similarity 76.6%; Pred. No. 3.5e-172;					
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;					
Qy	1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTFFR 45	Qy	1 MGR-----LLASALLC---VSGVFELKQEFVNKKGLL-NRNCRRGG-----GCCTFFR 45		
Db	1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR 60	Db	1 MGRRSALALAVVSALLCQVWSSGVFELKQEFVNKKGLLGNRNCRRGGSGPPCACRTFFR 60		
Qy	46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100	Qy	46 VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100		
Db	61 VCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120	Db	61 VCLKHYQASVSPEPPCTYGSATPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120		
Qy	101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVUDE 156	Qy	101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVUDE 156		
Db	121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180	Db	121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVUDE 180		
Qy	157 HYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209	Qy	157 HYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGC-DQHG-CDKPG 209		
Db	181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGOYCTDPICLPGCDDQHGYCDKPG 240	Db	181 HYGEGCSVFCRPRDDAFGHFTCGDRGKMCDPGWKGOYCTDPICLPGCDDQHGYCDKPG 240		
Qy	210 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268	Qy	210 ECKCRVWGQGRYCDICIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC-NG 268		
Db	241 ECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300	Db	241 ECKCRVWGQGRYCDICIRYPGCLHGTCQQPWQCNCQEGWGLFCNQDLNYCTHHKPCRNG 300		
Qy	269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCXNG-SCTDLES--SCTCPPGFYGK 317	Qy	269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCXNG-SCTDLES--SCTCPPGFYGK 317		
Db	301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSEKDEK 360	Db	301 ATCTNTGQGSYTCSCRPGYTGANCELEVDCAKSPCKNGASCTDLEDSEKDEK 360		
Qy	318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367	Qy	318 -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367		
Db	361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCPCPLGSGFNCEKKMDLCGSSPCSNKACV 420	Db	361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCPCPLGSGFNCEKKMDLCGSSPCSNKACV 420		
Qy	368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415	Qy	368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415		
Db	421 DLGNSYLCRCQAGFGRYCEDNVDDCASSPCANGGTCRDSVNDPFCCTCPPGYTKNCSAP 480	Db	421 DLGNSYLCRCQAGFGRYCEDNVDDCASSPCANGGTCRDSVNDPFCCTCPPGYTKNCSAP 480		
Qy	416 VSRCEH-PCNGATCHRR-----YCECA-GYGG-NCQFLLE-PPGP--VD-----EEQ- 458	Qy	416 VSRCEH-PCNGATCHRR-----YCECA-GYGG-NCQFLLE-PPGP--VD-----EEQ- 458		
Db	481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGGPNCQFLLEPPPPGPMVVDLSERHMSQG 540	Db	481 VSRCEHAPCHNGATCHQGRQRYMCECAQGYGGPNCQFLLEPPPPGPMVVDLSERHMSQG 540		
Qy	459 --FPM-AVCAGLV--LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANCOREK 503	Qy	459 --FPM-AVCAGLV--LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANCOREK 503		
Db	541 GPFPWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPPCGGETETMNNLANCOREK 600	Db	541 GPFPWAVACAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPPCGGETETMNNLANCOREK 600		
Qy	504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540	Qy	504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540		
Db	601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRLDKGDEATVRDTHSK 660	Db	601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRLDKGDEATVRDTHSK 660		
Qy	541 -----CSEKAL-----RKR-SPVYSTSKDTKYQSVYV--SEKDEC-IAT 576	Qy	541 -----CSEKAL-----RKR-SPVYSTSKDTKYQSVYV--SEKDEC-IAT 576		
Db	661 RDTKQSQSSAGEEKIAPTLLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720	Db	661 RDTKQSQSSAGEEKIAPTLLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720		
Qy	577 EV 578	Qy	577 EV 578		
Db	721 EV 722	Db	721 EV 722		
RESULT 4					

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Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCEKMDLGCSSPSCNGAKCV 420
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
QY 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
Db 481 VSRCEHAPCHNGATCHORQRYMCECAQYGGPNCFLLPEPPGPMVVDLSERHMESQG 540
QY 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANCQREK 503
Db 541 GPFPWAVACAGVVLVLLLLGCAA-VVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Db 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFVKRYPTVDYNLVRLDKGDEATVRDTHSK 660
QY 541 -----CSEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576
Db 661 RDTKCQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 5
AAR30869
ID AAR30869 PRELIMINARY; PRT; 722 AA.
AC AAR30869;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta like-1.
GN DLL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Nagaraja R., Waeltz P., Brathwaite M.E.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY497019; AAR30869.1; -
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 72.9%; Score 2466; DB 2; Length 722;
Best Local Similarity 76.6%; Pred. No. 3.5e-172;
Matches 553; Conservative 6; Mismatches 19; Indels 144; Gaps 71;

QY 1 MGR-----LLASALLC---VSGVFELKQEFVNNKGILL-NRNCRRG-----GCCTFFR 45
Db 1 MGRRSALALAVVSALLCQWSSGVFELKQEFVNNKGILLNRNCRRGSGSPPCACRTFFR 60
QY 46 VCLKHYQASVSPEPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100
Db 61 VCLKHYQASVSPEPCTYGSATPVLGVDSFSIPDGAGIDPAFSNPIRFPFGFTWPGTFS 120
QY 101 LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD 156
Db 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRSYRFVCD 180
QY 157 HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
Db 181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEMCDPGWKQGYCTDPICLPGCDDQHGYCDKPG 240
```

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QY 210 ECKCRVGWQGRYCDDECIRYPGCVHGTCCQPWCNCQEGWGLFCNQDLNYCTHHKPC-NG 268
Db 241 ECKCRVGWQGRYCDDECIRYPGCLHGTCCQPWCNCQEGWGLFCNQDLNYCTHHKPCRNG 300
QY 269 ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK 317
Db 301 ATCTNTGQGSYTCSCRPGYTGANCELEVEDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360
QY 318 -CELSAMTCADGPCFNGRC-DNPDGGY-C-CPLG-SGFNCEKGD--C-SSPC-NGA-CV 367
Db 361 VCELSAMTCADGPCFNGRCSDNPDGGYTCHCPLGFSGFNCEKMDLGCSSPSCNGAKCV 420
QY 368 DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
Db 421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
QY 416 VSRCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ- 458
Db 481 VSRCEHAPCHNGATCHORQRYMCECAQYGGPNCFLLPEPPGPMVVDLSERHMESQG 540
QY 459 --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK-----PE-C--ETETMNNLANCQREK 503
Db 541 GPFPWAVACAGVVLVLLLLGCAA-VVCVRLKLOKHQPPPEPCGGGETETMNNLANCQREK 600
QY 504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK 540
Db 601 DVSVSIIGATQIKNTNKKADFGHDHGAEKSSFVKRYPTVDYNLVRLDKGDEATVRDTHSK 660
QY 541 -----CSEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT 576
Db 661 RDTKCQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
QY 577 EV 578
Db 721 EV 722

RESULT 6
AAH65063
ID AAH65063 PRELIMINARY; PRT; 722 AA.
AC AAH65063;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
```







FT	DOMAIN	446	477	EGF-like 7, calcium-binding (Potential).
FT	DOMAIN	484	515	EGF-like 8.
FT	DISULFID	225	236	By similarity.
FT	DISULFID	229	242	By similarity.
FT	DISULFID	244	253	By similarity.
FT	DISULFID	256	267	By similarity.
FT	DISULFID	262	273	By similarity.
FT	DISULFID	275	284	By similarity.
FT	DISULFID	291	303	By similarity.
FT	DISULFID	297	313	By similarity.
FT	DISULFID	315	324	By similarity.
FT	DISULFID	331	342	By similarity.
FT	DISULFID	336	351	By similarity.
FT	DISULFID	353	362	By similarity.
FT	DISULFID	369	380	By similarity.
FT	DISULFID	374	390	By similarity.
FT	DISULFID	392	401	By similarity.
FT	DISULFID	408	419	By similarity.
FT	DISULFID	413	428	By similarity.
FT	DISULFID	430	439	By similarity.
FT	DISULFID	446	466	By similarity.
FT	DISULFID	468	477	By similarity.
FT	DISULFID	484	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	515	By similarity.
FT	CARBOHYD	476	476	N-linked (GlcNAc... ) (Potential).
SQ	SEQUENCE	714 AA;	77378 MW;	4B8EE2272BAEA27E CRC64;
Query Match 72.0%; Score 2436; DB 1; Length 714;				
Best Local Similarity 75.4%; Pred. No. 5.4e-170;				
Matches 538; Conservative 11; Mismatches 29; Indels 136; Gaps 66;				
QY	1	MGR-----LLASALLC----	VSGVFELKLQEFVNKKGLL-NRNCRRGG-----GCCTFFR	45
Db	1	MGRSALALAVVSALLCQWSSGVFELKLQEFVNKKGLLGNRNCRRGGSGPPCACTFFR	60	
QY	46	VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGTWPFTFS	100	
Db	61	VCLKHYQASVSPEPPCTYGSATVAVLGVDVSFLPDGAGIDPAFSNPIRFPFGTWPFTFS	120	
QY	101	LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCD	156	
Db	121	LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEWSQDLHSSGRTDLRYSYRFVCD	180	
QY	157	HYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGYCT-PICLPGC-DHGG-CDKPG	209	
Db	181	HYGEGCSVFCRPRDDAFGHFTCGERGEKMDPGWKGYCTDPICLPGCDDHGGYCDKPG	240	
QY	210	ECKRVGWQGRYCDJCIRYPCGVHGTQQPWCNQCNQEGWGLFCNQDLNYCTHHKPC-NG	268	
Db	241	ECKRVGWQGRYCDJCIRYPCGLHGTQQPWCNQCNQEGWGLFCNQDLNYCTHHKPCRN	300	
QY	269	ATCTNTGQSYTCSRPYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYK	317	
Db	301	ATCTNTGQSYTCSRPYTGANCELEVDECAPSPCRNGSGCTDLEDYSYCTCPPGFYK	360	
QY	318	-CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CV	367	
Db	361	VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGPSGFNCEKKIDLCSSSPCSNGAKCV	420	
QY	368	DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P	415	
Db	421	DLGNSYLCRCQTGFSGRYCEDNVDDCASSPCANGTCRDSVDFSCTCPPTGRNCSAP	480	
QY	416	VSRCEH-PCHNGATCHRR---YCECA-GYGG-NQCFLLPEPPGPV----DEEQFPW-AV	463	
Db	481	VSRCEHAPCHNGATCHRGQRYMCECAQGYGGANCQFLPEPPPDLVAAQGSFPWVAV	540	
QY	464	CAGLV---LLLLGCAA-VVVRLLK---QKP--EC--ETETMNNLANCQREKD---SSIG	508	
Db	541	CAGVLVLLLLLGGCAAVVVVRLLKLQKHQPPPPCGGETETMNNLANCQREKDVSVIIG	600	
QY	509	ATQIKNTNKK-DFH-----DK---KVRYP-VDYNLV-----LKVHKKC---	541	

Db	601	ATQIKNTNKKADFHGDHGDSSFKARYPTVDYNLIRDLKGDEATVRDAHSKRDTKCQSQ	660	
QY	542	---SEEKAL-----RKRP-SVYSTSKDTKYQSVVV--SEKDEC-IATEV	578	
Db	661	GSVGEKSTSTLRGGEVDPDRKPESVYSTSKDTKYQSVVLSAEKDECIVATEV	714	
RESULT 8				
DL11_HUMAN				
ID	DL11_HUMAN	STANDARD;	PRT;	723 AA.
AC	O00548; Q9NU41; Q9UUV2;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)			
DE	(H-Delta-1) (UNQ146/PRO172).			
GN	Name=DL11;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99180765; PubMed=10079256;			
RA	Gray G.S., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,			
RA	Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;			
RT	"Human ligands of the Notch receptor.";			
RL	Am. J. Pathol. 154:785-794(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han W., Ye Q., Moore M.A.S.;			
RT	"A soluble form of human delta-like-1 inhibits differentiation of			
RT	hematopoietic progenitor cells.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Oda T., Chandrasekharappa S.C.;			
RT	"Human Delta 1 gene sequence.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Almeida J.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	FUNCTION.			
RX	MEDLINE=21464863; PubMed=11581320;			
RA	Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,			
RA	Henrique D., Parreira L.;			
RT	"Differential effects of Notch ligands Delta-1 and Jagged-1 in human			
RT	lymphoid differentiation.";			
RL	J. Exp. Med. 194:991-1001(2001).			
CC	-I- FUNCTION: Acts as a ligand for Notch receptors. Blocks the			
CC	differentiation of progenitor cells into the B-cell lineage while			
CC	promoting the emergence of a population of cells with the			
CC	characteristics of a T-cell/NK-cell precursor.			
CC	-I- SUBUNIT: Interacts with Notch receptors.			

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower  
CC expression in brain and muscle and almost no expression in  
CC placenta, lung, liver, and kidney.  
CC -!- SIMILARITY: Contains 1 DSL domain.  
CC -!- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
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CC -----  
DR EMBL; AF003522; AAB61286.1; -.  
DR EMBL; AF196571; AAF05834.1; -.  
DR EMBL; AF222310; AAG09716.1; -.  
DR EMBL; AY358892; AAQ89251.1; -.  
DR EMBL; AL078605; CAB89569.1; -.  
DR HSSP; P00740; 1EDM.  
DR Genew; HGNC:2908; DLL1.  
DR MIM; 606582; -.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005112; P:Notch binding; IPI.  
DR GO; GO:0030154; P:cell differentiation; TAS.  
DR GO; GO:0001709; P:cell fate determination; NAS.  
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.  
DR GO; GO:0009912; P:hair cell fate commitment; ISS.  
DR GO; GO:0030097; P:hemopoiesis; NAS.  
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.  
DR GO; GO:0007399; P:neurogenesis; ISS.  
DR GO; GO:0007219; P:Notch signaling pathway; NAS.  
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.  
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR00742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS50026; EGF\_3; 7.  
DR PROSITE; PS01187; EGF\_CA; 1.  
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
KW Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 723 Delta-like protein 1.  
FT DOMAIN 18 545 Extracellular (Potential).  
FT TRANSMEM 546 568 Potential.  
FT DOMAIN 569 723 Cytoplasmic (Potential).  
FT DOMAIN 159 221 DSL.  
FT DOMAIN 226 254 EGF-like 1.  
FT DOMAIN 257 285 EGF-like 2.  
FT DOMAIN 292 325 EGF-like 3.  
FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).  
FT DOMAIN 370 402 EGF-like 5.  
FT DOMAIN 409 440 EGF-like 6.  
FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).  
FT DOMAIN 485 516 EGF-like 8.  
FT DISULFID 226 237 By similarity.  
FT DISULFID 230 243 By similarity.  
FT DISULFID 245 254 By similarity.  
FT DISULFID 257 268 By similarity.  
FT DISULFID 263 274 By similarity.

FT	DISULFID	276	285	By similarity.
FT	DISULFID	292	304	By similarity.
FT	DISULFID	298	314	By similarity.
FT	DISULFID	316	325	By similarity.
FT	DISULFID	332	343	By similarity.
FT	DISULFID	337	352	By similarity.
FT	DISULFID	354	363	By similarity.
FT	DISULFID	370	381	By similarity.
FT	DISULFID	375	391	By similarity.
FT	DISULFID	393	402	By similarity.
FT	DISULFID	409	420	By similarity.
FT	DISULFID	414	429	By similarity.
FT	DISULFID	431	440	By similarity.
FT	DISULFID	447	467	By similarity.
FT	DISULFID	469	478	By similarity.
FT	DISULFID	485	496	By similarity.
FT	DISULFID	490	505	By similarity.
FT	DISULFID	507	516	By similarity.
FT	CARBOHYD	477	477	N-linked (GlcNAc... ) (Potential).
FT	CONFLICT	498	498	E -> Q (in Ref. 2).
FT	CONFLICT	502	502	G -> R (in Ref. 4 and 5).
FT	CONFLICT	510	510	G -> S (in Ref. 2).
SQ	SEQUENCE	723 AA;	77956 MW;	B4EC455FFA32A12B CRC64;

Query Match 71.0%; Score 2401.5; DB 1; Length 723;  
Best Local Similarity 75.1%; Pred. No. 1.8e-167;  
Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps 67;

Qy	7	SALLC---	VSGVFELKIQEFVNKKGLL-NRNCRRG-----GCCTFFRVCLKHQASVS	56
Db	13	SALLCQVWSSGVFELKIQEFVNKKGLLGNRNCRRGAGPPPCACRTFFRVCLKHQASVS	72	
Qy	57	PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP	111	
Db	73	PEPPCTYGSATPVLGVDSFSLPDGGADSAFSNPIRFPFGFTWPGTFSLIIEALHTDSP	132	
Qy	112	DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRDLYSYRVCDEHYHGGCSVFC	167	
Db	133	DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRDLYSYRVCDEHYHGGCSVFC	192	
Qy	168	RPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPgcd-QHG-CDKPGECKCRVGWQGR	220	
Db	193	RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPgcdeQHGFCDKPGECKCRVGWQGR	252	
Qy	221	YDECIRYPGCVHGTCCQPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY	279	
Db	253	YDECIRYPGCLHGTCQQPWCNCQEGWGLFCNQDLNYCTHHKPCNGATCTNTGQGSY	312	
Qy	280	TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFGYK-CELSAMTCAD	327	
Db	313	TCSCRPGYTGATCELGIDCDSPSPCKNGSGCTDLENSYSCTCPPGYGKICELSAMTCAD	372	
Qy	328	GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNYS-C-CQ	376	
Db	373	GPCFNGGRCSDSPDGGYSCRCPCVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ	432	
Qy	377	AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN	425	
Db	433	AGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSTCTPPGYTGRNCSAPVSRCEHAPCHN	492	
Qy	426	GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL	467	
Db	493	GATCHERGHGVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPVAVCAGV	552	
Qy	468	VL---LLLGCAA-VVCVRL---KQKPEC-----ETETMNNLANCQREK---SSIGATQI	512	
Db	553	ILVLMLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKISVSIIGATQI	612	
Qy	513	KNTNKK-DFH-----DK---KVRY-PVDYNLV-----LKVHKC-----S	542	
Db	613	KNTNKKADFHGHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPGSSG	672	
Qy	543	EEKAL-----RKRPP-SVYSTSKDTKYQSVVY--SEKDEC-IATEV	578	

Db	673	EEKGTPTTLRGGEASERKRPSDSCSTSKDTKYQSVYVISEEKDECVIATEV	723
RESULT 9			
Q8AW87			
ID	Q8AW87	PRELIMINARY;	PRT; 726 AA.
AC	Q8AW87;		
DT	01-MAR-2003	(TrEMBLrel. 23, Created)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Ligand Delta-1.		
GN	Name=Delta-1;		
OS	Cynops pyrrhogaster (Japanese common newt).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.		
OX	NCBI_TaxID=8330;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: Contains 8 EGF-like domains.		
DR	EMBL; AB095017; BAC41350.2; -.		
DR	HSSP; P00740; 1EDM.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0007154; P:cell communication; IEA.		
DR	InterPro; IPR000152; Asx_hydroxyl_S.		
DR	InterPro; IPR001774; DSL.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR001438; EGF_II.		
DR	InterPro; IPR006209; EGF_like.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 6.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00181; EGF; 8.		
DR	SMART; SM00179; EGF CA; 6.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.		
DR	PROSITE; PS00022; EGF_1; 8.		
DR	PROSITE; PS01186; EGF_2; 7.		
DR	PROSITE; PS50026; EGF_3; 6.		
DR	PROSITE; PS01187; EGF_CA; 2.		
KW	EGF-like domain.		
SQ	SEQUENCE 726 AA; 79866 MW; 352A40219AE67F41 CRC64;		
Query Match			
Best Local Similarity 67.0%; Score 2267.5; DB 2; Length 726;			
Matches 496; Conservative 23; Mismatches 56; Indels 145; Gaps 58;			
QY	4	LLASALLCV-----SGVFELKLOEFVKKGLL-NRNCRRGG-----CCTFFR	45
Db	7	LACAAALLCVLCQVSCSGVFELKLOEFVKKGLGNANCCRAGGSVQQGALLQCQCRTFR	66
QY	46	VCLKHYQASVSPBPCTYGSA-TPVL--GSFSPDGAGDPAFSNPIRPFPGFTWPGTFSLI	102
Db	67	VCLKHYQANVSPEPCTYGSVTPVLQGSFTVPEGGEATFSNPIRIFAFTWPGTFSLI	126
QY	103	IEALHTDSPDDL-TENPERLISRLT-QRHL-VGEEWSQDLHSSGRITDL-YSYRFVCDHEY	158
Db	127	IGALHTDSPDDLSTENPDRLISRMAIQRHLAVGEDWSQDSQSSGRITDLKYSYRFVCDHEY	186
QY	159	YGEGCSVFRCPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC	211
Db	187	YGEGCSVFRCPRDDTFGHFTCGERGEKQCNQGWKGQYCTEAILCPGDEQHGFCDRPGEC	246
QY	212	KCRVGMQGRYDCIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNCTTHHKPC-NGAT	270
Db	247	KCRVGMQGRYDCIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNCTTHHKPCNAAT	306
QY	271	CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGYGK-C	318

Db	307	CTNTGQGSYTCSCRPGYTGANCEIEVNECEASPCCKNGGSCADLENSYSCSPPGYGNK	366
QY	319	ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFENCEK--DCSS-PC-NGA-CVDL	369
Db	367	ELSAMTCADGPCFNGGRCSDNPEGGYSCRCPLSYSGFENCEKKIDYCSSNPGNCAHCVDL	426
QY	370	GSNYCCQA--GF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS	417
Db	427	GSNYICQCLDGFSGRHCDNLDDCASYPCANGGTCDGVNDYSCTCPPGYNGKNCSTPVS	486
QY	418	RCEH-PCHNGATCHRR-----YCECA-GYGG-NCQFLLPEPPGPVDE-----EQ	458
Db	487	RCEHSPCHNGATCHERNRNVCECARGYGLNCQFLLPEQPQEHDTGDNTEKYTEDQGGQ	546
QY	459	FPW-AVCAGLVL---LLLGCAA-VVCVRLKQKPE-----CETETMNNLANCQREKD	504
Db	547	FPWIAVCAGIILVLMLLFGCAAVVCFRLKMHKQQRQSDSYRGESETMNNLANCRREK	606
QY	505	---SSIGATQIKNTNKK-----DFHDKKVRYP-VDYNLVL-----KVH	538
Db	607	ISVSVIGATQIKNTNKKADLYSESTDKNYKARYPSVDYNLVHELKHEDSVKEEHGKRE	666
QY	539	KKC-----SEEKALRKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV	578
Db	667	SKCIANGSEADEKHPVLKSSSETSERRPESLYSTKETYQSVYVISEAKDECIATEV	726
RESULT 10			
Q91902			
ID	Q91902	PRELIMINARY;	PRT; 721 AA.
AC	Q91902;		
DT	01-NOV-1996	(TrEMBLrel. 01, Created)	
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	X-Delta-1.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95319507; PubMed=7596411;		
RA	Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;		
RT	"Expression of a Delta homologue in prospective neurons in the		
RT	chick."		
RL	Nature 375:787-790(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95319503; PubMed=7596407;		
RA	Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;		
RT	"Primary neurogenesis in Xenopus embryos regulated by a homologue of		
RL	the Drosophila neurogenic gene Delta."		
RL	Nature 375:761-766(1995).		
DR	EMBL; L42229; AAC38017.1; -.		
DR	HSSP; P00740; 1EDM.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0007154; P:cell communication; IEA.		
DR	InterPro; IPR000152; Asx_hydroxyl_S.		
DR	InterPro; IPR001774; DSL.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR001438; EGF_II.		
DR	InterPro; IPR006209; EGF_like.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 6.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00179; EGF CA; 4.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.		
DR	PROSITE; PS00022; EGF_1; 8.		



DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS50026; EGF_3; 6.	
DR	PROSITE; PS01187; EGF_CA; 2.	
KW	EGF-like domain.	
SQ	SEQUENCE 721 AA; 79922 MW; 9BBD85C439DD194 CRC64;	
Query Match 66.9%; Score 2262.5; DB 2; Length 721;		
Best Local Similarity 68.7%; Pred. No. 2.8e-157;		
Matches 489; Conservative 39; Mismatches 47; Indels 137; Gaps 61;		
Qy	4 LLASALLC---VSGVFELKQEFVNKKGLL-NRNCCRGG-----CCTFFRVCLKHY 51	
Db	10 LVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCRCPSLASLQRCCECKTFFRICLKHY 69	
Qy	52 QASVSPEPPCTYGSA-TPVLGSFS---PDGA-GDPAFNSPIRFPFGFTWPGTFSLIEAL 106	
Db	70 QSNVSPEPPCTYGGAVTPVLGTSFVVPESSNADPTFSNPDIRFPFGFTWPGTFSLIEAI 129	
Qy	107 HTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHYVYEG 162	
Db	130 HADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSYRFVCDHYVYEG 189	
Qy	163 CSVFECRPRDD-FGHFTCG-RGEK-C-PGWKGOYCT-PICLPGCCDHG--CDKPGECKRV 215	
Db	190 CSDYCRPRDDAFGHFSCGEKELCNPGWKGLYCTEPICLPGCDEHHGYCDKPGECKRV 249	
Qy	216 GWQGRYCDICIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPC-NGATCTNT 274	
Db	250 GWQGRYCDICIRYPGCLHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCENGATCTNT 309	
Qy	275 GQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLESS--CTCPPGFGYK-CELSA 322	
Db	310 GQGSYTCSCRPGYTGSNCEIEVNECDANPCKNGGSCSDLENSYTCSCPPGFGYKNCLESA 369	
Qy	323 MTCADGPCFNGGRC-DNPDDGY-C-CPLG-SGFNCEKK--DCSS-PC-NGA-CVDLGSY 373	
Db	370 MTCADGPCFNGGRCADNPDDGYICFCPVGYSGFNCEKKIDYCSSNPCANGARCEDLGSY 429	
Qy	374 CCOA--GF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVSRCEH 421	
Db	430 ICQCQEGFSGRNCDDNLDCTSPFCQGGTQCQDGINDVSCTCPGPGYIGKNCSPITKCEH 489	
Qy	422 -PCHNGATCHRR----YCECA-GYGG-NCQFLLP-EPPGPVD-----EEQFPW-AV 463	
Db	490 NPCHNGATCHERNRYVQCARGYGNNCQFLLPPEKPVVVDLTEKYTEGQSGQPWIAV 549	
Qy	464 CAGLVL---LLLGCA-VVCVRL-----KQKPEC---ETETMNNLANCQREK----SSIG 508	
Db	550 CAGIVLVMLLLGCAVVVCRVRVQKRRHQPEACRGESKTMNNLANCQREKDLSVSFIG 609	
Qy	509 ATQIKNTNKK-DF-----HDKKVRYP-VDYNLV-----LKVHKKS--- 542	
Db	610 TTQIKNTNKKIDFLSESNNERNKYKPRYPVDYNLVHELKNEDSPKEERSKCEAKCSSND 669	
Qy	543 -----EEKALRKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578	
Db	670 SDESDVNSVHSKRDSERRRPSAYSTSKDTKYQSVYVISDEKDECIIATEV 721	

RESULT 11  
Q8UWJ4  
ID Q8UWJ4 PRELIMINARY; PRT; 720 AA.  
AC Q8UWJ4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DeltaD protein.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]

RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22248969; PubMed=12361969;	
RA	Hans S., Campos-Ortega J.A.;	
RT	"On the organisation of the regulatory region of the zebrafish deltaD gene.";	
RL	Development 129:4773-4784(2002).	
DR	EMBL; AF426384; AAL31528.1; --.	
DR	HSSP; P00740; 1EDM.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0005509; F:calcium ion binding; IEA.	
DR	GO; GO:0007154; P:cell communication; IEA.	
DR	InterPro; IPR000152; Asx_hydroxyl_S.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_II.	
DR	InterPro; IPR006209; EGF_like.	
DR	Pfam; PF01414; DSL; 1.	
DR	Pfam; PF00008; EGF; 6.	
DR	PRINTS; PR00010; EGFBL00D.	
DR	SMART; SM00051; DSL; 1.	
DR	SMART; SM00179; EGF_CA; 4.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.	
DR	PROSITE; PS00022; EGF_1; 8.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS50026; EGF_3; 6.	
DR	PROSITE; PS01187; EGF_CA; 2.	
KW	EGF-like domain.	
SQ	SEQUENCE 720 AA; 79380 MW; DE6B7393E2AA0FE6 CRC64;	
Query Match 61.6%; Score 2084.5; DB 2; Length 720;		
Best Local Similarity 63.4%; Pred. No. 3e-144;		
Matches 456; Conservative 51; Mismatches 69; Indels 143; Gaps 59;		
Qy	1 MGRLLASALLCV-----SGVFELKQEFVNKKGLL-NRNCCRGG-----CCTFFR 45	
Db	1 MGRLMIAVLLCVMISQGPCSGVFELKQEFLNKKVGTGNANCKGSAAEHQCECKTFFR 60	
Qy	46 VCLKHYQASVSPEPPCTYGSA-TPVLGSFS---PDGAGDPAFNSPIRFPFGFTWPGTFSL 101	
Db	61 ICLKHYQANVSPDPCTYGGAVTPVLGSNSFQVPDSFPDSSFTNPIPFAFGFTWPGTFSL 120	
Qy	102 IIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRTDL-YSYRFVCDHEH 157	
Db	121 IIEALHTDSTDDLSTENPDRLISRMTTQRHLTVGEWSQDLQVGRTELKYSYRFVCDHEH 180	
Qy	158 YYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKGOYCT-PICLPGCCDQ-HG-CDKPGE 210	
Db	181 YYGEGCSVFCRPRDDTFGHFTCGERGEIICNSGWKGOYCTEPICLPGCDEDHGFCDKPGE 240	
Qy	211 CKCRVWQGRYCDICIRYPGCVHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPC-NGA 269	
Db	241 CKCRVGFSGKYCDDCIRYPGLHGTCCQPPWCNCQEGWGLFCNQDLNYCTHHKPCQNGA 300	
Qy	270 TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFGYK- 317	
Db	301 TCTNTGQGSYTCSCRPGTGDSCIEVNECSGSPCRNGGSCDLENTYSCTCPPGFGYGRN 360	
Qy	318 CELSAMTCADGPCFNGGRC-DNPDDGY-C-CPLG-SGFNCEKK--DCSS-PC--NGACVD 368	
Db	361 CELSAMTCADGPCFNGGHGHCADNPEGGYFCQCPMGYAGFNCEKKIDHCSSNPCSNDQAQILD 420	
Qy	369 LGNSYCCQAGFG----RC-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNC-SPV 416	
Db	421 LVDSYLCQCPEGFTGTHCEDNIDECATYPCQNGGTQDQGLSDYCTCTCPPGYTGKNCCTSAV 480	
Qy	417 SRCEH-PCHNGATCH---RRYCEC-AGYGG-NCQFLLPE-PPGPV-----D 455	
Db	481 NKCLHNPCHNGATCHENDNRVVCACIPYGGRNQFLLPENPQQAIVEGADKRYSEED 540	
Qy	456 EEQFPW-AVCAGLVLLLL-----GCAAVVCVRLKQK-----PECETETMNNLANCO-RE 502	
Db	541 DGGFPWTAVCAGIILVLLVLIGGSVFVIYIRLKLQORSQQIDSHSEIETMNNLTNRSRE 600	



QY 503 KD---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKVHK----- 539  
DB 601 KDLVSIIGATQVKININKKVDVDFQSDGDKNGFKSRYSLVVDYNLVHELKQEDLGKEDSERSE 660  
QY 540 --KC-----SEEK-----ALRKRPVSVYSTKTKYQSVYV--SEKDEC-IATEV 578  
DB 661 ATKCEPLDSDSEKHRNHLKSDSERK RTE--SLCKDTKYQSVFVLSSEKDECIATEI 717

RESULT 12  
P87357 ID P87357 PRELIMINARY; PRT; 717 AA.  
AC P87357  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DeltaD transmembrane protein precursor.  
GN Name=dld; Synonyms=deltad;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97346722; PubMed=9203139;  
RA Dornseifer P., Takke C., Campos-Ortega J.A.;  
RT "Overexpression of a zebrafish homologue of the Drosophila neurogenic  
RT gene delta perturbs differentiation of primary neurons and somitic  
RT development.";  
RL Mech. Dev. 63:159-171(1997).  
DR EMBL; Y11760; CAA72425.1; -.  
DR HSPF; P00740; IEDM.  
DR ZFIN; ZDB-GENE-990415-47; dld.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGFBLD.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS00026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW EGF-like domain; Signal; Transmembrane.  
FT SIGNAL . 4 11 Potential.  
SQ SEQUENCE 717 AA; 79061 MW; 9C5A0162504593E4 CRC64;

Query Match 61.5%; Score 2081.5; DB 2; Length 717;  
Best Local Similarity 63.4%; Pred. No. 5e-144;  
Matches 456; Conservative 51; Mismatches 69; Indels 143; Gaps 59;

QY 1 MGRLLASALLCV-----SGVFELKQEFVNNKGLL-NRNCRCGG-----CCTFFR 45  
DB 1 MGRLMIAVLLCMISQGFCSGVFELKQEFLNKKGVGTGNANCCGSAABGHQCECKTFFR 60  
QY 46 VCLKHYQASVSPPPCTYGSA-TPVLGSFS--PDGAGDPAFNSPIRFPFGFTWPGTFSL 101  
DB 61 ICLKHYQANVSPDPCTYGGAVTPVLGSNSFQVPESFPDSSFTNPFPAGFTWPGTFSL 120  
QY 102 IIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEWSQDLHSSGRDIL-YSYRFVCDL 157  
DB 121 IIEALHTDSTDLDSTENPDRLISRMTTQRHLTVGEWSQDLQVGGRTLKYSYRFVCDL 180

QY 158 YYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKGQYCT-PICLPGCDQ-HG-CDKPGE 210  
DB 181 YYGEGCSVFCRPRDDTGHFTCGERGEIICNSGWKGQYCTEPICLPGCDEDHGFCDKPGE 240  
QY 211 CKCRVGMQGRVCDICIRYPGCVHGTCCQWQNCQEGWGLFCNQDLNYCTHHKPC-NGA 269  
DB 241 CKCRVGFSGKYCDDCIRYPGCLHGTCCQWQNCQEGWGLFCNQDLNYCTHHKPCQNGA 300  
QY 270 TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPGPFYGK- 317  
DB 301 TCTNTGQGSYTCSCRPGFTGDSCEIEVNECSGSPCRNGGSCDTLENTYSCTCPGFGYGRN 360  
QY 318 CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSS-PC--NGACVD 368  
DB 361 CELSAMTCADGPCFNGGHCADNPEGGYFCQCPMGYAGFNCEKKIDHCSSNPCSNDACQLD 420  
QY 369 LGNSYCCQAGFG----RC-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNC-SPV 416  
DB 421 LVDSYLCQCPGFTGTHCEDNIDECATYPCQNGGTCQDGLSDYTCTCPPGYTGKNCCTSAV 480  
QY 417 SRCEH-PCHNGATCH---RRYCEC-AGYGG-NCQFLLE-PPGPV-----D 455  
DB 481 NKCLHNPCHNGATCHEMDNRYVCACIPGYGGRNCQFLPENPQQAIVEGADKRYSEED 540  
QY 456 EEQFPW-AVCAGLVLLL---GCAAVVCVRLKQK-----PECETETMNNLANCQ-RE 502  
DB 541 DGGFPWTAVCAGIILVLLVLIGGSVFYIIRLKLQORSQQIDSHSEIETMNNLTNRSRE 600  
QY 503 KD---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKVHK----- 539  
DB 601 KDLVSIIGATQVKININKKVDVDFQSDGDKNGFKSRYSLVVDYNLVHELKQEDLGKEDSERSE 660  
QY 540 --KC-----SEEK-----ALRKRPVSVYSTKTKYQSVYV--SEKDEC-IATEV 578  
DB 661 ATKCEPLDSDSEKHRNHLKSDSERK RTE--SLCKDTKYQSVFVLSSEKDECIATEV 717

RESULT 13  
Q6DI48 ID Q6DI48 PRELIMINARY; PRT; 772 AA.  
AC Q6DI48;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075742; AAH75742.1; -.
KW Hypothetical protein.
SQ SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;

Query Match      59.5%; Score 2014; DB 2; Length 772;
Best Local Similarity 58.4%; Pred. No. 4.8e-139;
Matches 452; Conservative 48; Mismatches 76; Indels 198; Gaps 61;

QY 1 MGR-----LLAS---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCC 41
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Db 1 MGRHLLLLLSILYMLLCQASSSGVFELKQEFLNKKGVQGNKNCCKGGLTTSYQOCECK 60

QY 42 TFFRVCLKHYQASVSPEPPCTY-GSATPVLGSFS---PDGAGDPAFSNPIRFPFGTWP 97
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Db 61 TFFRICLKHYQPNASPEPPCTYGGTVTPVLGSNSFQVDTLPDGSFTNPIRMNFGTWP 120

QY 98 TFSLIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFV 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TFSLIIEALHADSKEDLT TENPERII STMTTQRHLTVGEDWSQDLHSVGRTELKYSYRFV 180

QY 154 CDEHYYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKQGYCT-PICLPGCD-QHG-CD 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CDEHYYGEGCSVFCRPRDDAFGHFTCGERGEIICDAGWKQGYCTEPICLPGCDEEHGFC 240

QY 207 KPGECKCRVWGQGRYCDCEIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 KPGECKCRVFGKGRYCDCEIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC 300

QY 267 -NGATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGF 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 LNGATCSNTGQGSYTCSCRPGFSGASCEIEVNECTGNPCRNGGSCDTMENTYSCTCPPGF 360

QY 315 YGK-CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DC-SSPC-NGA 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 YGKNCELSAMTCADGPCFNGGRCADNPDGGYFCQCPTGYAGFNCEKKIDHCSSSPCSNGA 420

QY 366 -CVDLGN SYCCQAGFG----RCDNV-DDCAS-PC-NGGTCDVNDS---CTCPPGY-GKNC 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 RCVDLVNSYLCQCPDGF TGMNCDRAGDECSMYPCQNGGTCQEGASGYMCTCPPGYTGRNC 480

QY 414 -SPVSRCEH-PCHNGATCHRR----YCEC-AGYGG-NCQFLLPEPPGPVDEEQFPW-AVC 464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 SSPVSRCOHNPCHNGATCHERNRNVYCACVSGYGGRCNQFLLPDRASQIASD-VPWTAVG 539

QY 465 AGLVLLLL--GCA-AVVCVRLK-----QKPECETETMNNLA-NCQREKD---SS 506
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 SGVLLVLLLVACAVVVCVRSKVQORRRDREREDEVANGENETINNLTNNCHRDKDLAVSV 599

QY 507 IGATQIKNTNKK-DF---HDK-----KVRYPVDYNLV----- 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 600 VGVAPVKNINKKIDFSSDHDLSLTTEKRSYKTRHAPADYNLVHEVKFEVKEVKLEHAG 659

QY 535 -----LVKHKKCSEEKALRKR----- 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 KETTMANELSDSCEDIKQSLQDSSECTEER-RKRLKSDASEKSKYSESRYSESKYSES 718

QY 553 VYSTSK-----DTKYQSYVYV--SEKDEC-IATEV 578
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Db 719 KYSEKYSVDVLSYESACASACASASTSACVDTKYKSVVMVMSSEKDECVIATEV 772

RESULT 14
O57462
ID O57462 PRELIMINARY; PRT; 802 AA.
AC O57462;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DeltaA.
GN Name=dla; Synonyms=deltaA;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98165392; PubMed=9425133;
RA Appel B., Eisen J.S.;
RT "Regulation of neuronal specification in the zebrafish spinal cord by
   Delta function.";
RL Development 125:371-380(1998).
DR EMBL; AF030031; AAC41249.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-980526-29; dla.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 802 AA; 88941 MW; 0D8A9734585918E5 CRC64;

Query Match      58.8%; Score 1989.5; DB 2; Length 802;
Best Local Similarity 60.4%; Pred. No. 3.1e-137;
Matches 442; Conservative 51; Mismatches 80; Indels 159; Gaps 61;

QY 1 MGR-----LLAS---VSGVFELKQEFVNKKGLL-NRNCRRG-----GCC 41
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Db 39 MGRHLLLLLSILYMLLCQASSSGVFELKQEFLNKKGVQGNKNCCKGGLTTSYQOCECK 98

QY 42 TFFRVCLKHYQASVSPEPPCTY-GSATPVLGSFS---PDGAGDPAFSNPIRFPFGTWP 97
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 TFFRICLKHYQPNASPEPPCTYGGTVTPVLGSNSFQVDTLPDGSFTNPIRMNFGTWP 158

QY 98 TFSLIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFV 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 TFSLIIEALHADSKEDLT TENPERII STMTTQRHLTVGEDWSQDLHSVGRTELKYSYRFV 218

QY 154 CDEHYYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKQGYCT-PICLPGCD-QHG-CD 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 CDEHYYGEGCSVFCRPRDDAFGHFTCGERGEIICDAGWKQGYCTEPICLPGCDEEHGFC 278

QY 207 KPGECKCRVWGQGRYCDCEIRYPGCVHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 KPGECKCRVFGKGRYCDCEIRYPGCLHGTCCQPPWQCNCQEGWGLFCNQDLNYCTHHKPC 338

QY 267 -NGATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGF 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 LNGATCSNTGQGSYTCSCRPGFSGASCEIEVNECTGNPCRNGGSCDTMENTYSCTCPPGF 398

QY 315 YGK-CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DC-SSPC-NGA 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 YGKNCELSAMTCADGPCFNGGRCADNPDGGYFCQCPTGYAGFNCEKKIDHCSSSPCSNGA 458
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QY 366 -CVDLGNISYCCQAGFG-----RCDNV-DDCAS-PC-NGGTCDVNDS---CTCPPGY-GKNC 413  
Db 459 RCVDLVNSYLQCPCPDGFTGMNCDRAGDECSMPYPCQNGGTCQEGASGYMCTCPPGYTGRNC 518  
QY 414 -SPVSRCEH-PCNHGATCHRR-----YCEC-AGYGG-NCQFLLPEPPGPFVDEQPFM-AVC 464  
Db 519 SSPVSRQCNPCHNGATCHERNRYVCACVSGYGGRCQFLLPDRASQIASD-VPWTAVG 577  
QY 465 AGLVLLLL---GCA-AVVCVRLK-----QKPECETETMNNLA-NCQREKD---SS 506  
Db 578 SGVLLVLLLVACAVVVVRSKVVQRRRRDRREDEVANGENETINNLTNNCHRDLDLAVSV 637  
QY 507 IGATQIKNTNKK-DF---HDK-----KVRY-PVDYNLV----- 534  
Db 638 VGVAPVKNINKIDFSSDHDLSLTTEKRSYKTRHAPADYNLVHEVKFEVKHEVKLEHAG 697  
QY 535 -----LKVHKKCSEKALRKR-----PSVYSTSK--DTKY-QS 564  
Db 698 KETTMANELSDSCEDIKQSLQDSSECTEKR-RKRLKSDASEKSKYSESRYSESKYSES 756  
QY 565 VYVSEK-DECIA 575  
Db 757 KYSEKYSRCIA 768  
RESULT 15  
Q7ZXT4  
ID Q7ZXT4 PRELIMINARY; PRT; 642 AA.  
AC Q7ZXT4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MGC52561 protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
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RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC044262; AAH44262.1; --  
DR HSSP; P00740; 1EDM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007154; P:cell communication; IEA.  
DR InterPro; IPR000152; Aax\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 1.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 3.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 2.  
KW EGF-like domain.  
SQ SEQUENCE 642 AA; 70655 MW; 56AFB4013E1C2AE2 CRC64;  
Query Match 40.9%; Score 1383; DB 2; Length 642;  
Best Local Similarity 46.3%; Pred. No. 6.4e-93;  
Matches 310; Conservative 74; Mismatches 151; Indels 134; Gaps 48;  
QY 7 SALLCV-----SGVFELKLOEFVNKKGLLNRNCCRGCGCCTFFRVCLKHQASVSPEPPC 61  
Db 11 AATLCPLVYPAGVFELKIHFSFTRPA-----CAAGKSCNIFFRVCLKHAQPVVSPDPPC 66  
QY 62 TYGSATPVLGSFSPDGAGDPAFNSPIRPFPGFTWPGTFSLIIEALHTDSPDLTENPERL 121  
Db 67 TFGSA--VSDILPDSKAITDSSPIRVPFPHFKWPGIFSLIIESWTTNSAEQSTENPDNL 123  
QY 122 ISRL-TQRHL-VGEESQDLHSSGRTDL-YSYRFVCDHYHGGCVFCRPRDD-FGHFT 177  
Db 124 LSLATRRRLSIGEDWSQDIHLGQSELRYSYHVSVCDEHYHGDSCDYCRPRDNFGHYT 183  
QY 178 C---GRGEKCPGWKGYCT-PICLPGC-DQHG-CDKPGECKRQVWQGRYQDCDECIRYPGC 231  
Db 184 CDEQGNRLCMWSGWKGEYCAEPICLPGCSHGFCELPGECKCRMGWQGLCDECLRYPGC 243  
QY 232 VHGTQQPWCNQCQEGWGLFCNQDLNYCTHHKPC-NGATCTNTGGSYTCSCRPGYTG- 289  
Db 244 QHGSCSQPWCICQEGWGLFCNQDLNYCTNHQPCRNAGASCINTGGSYSCSCLAGTGT 303  
QY 290 -CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTADGCPFNNGRCND 338  
Db 304 NCEIDINECASNPCKNGGSCNDLENDYECVCPRGFYGKNCDISAMTCEGCPFNNGGTG 363  
QY 339 PDGG---YC-CPLG-SGFNCEKK--DC-SSPC--NGACVDLG-NSYC-COAGFG--RCD- 383  
Db 364 KSSGVGYVCRCPFNHYHGSNCEKKIDRCTNSPCLNGGQCLDMGRNVLCRPGFSGPRCEL 423  
QY 384 NVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRG-EHPCHNGATCHRRY-- 433  
Db 424 NIDDCASSPCANGGTCVDAVNSYTCSTLGYGKDKCTLRVDACSSKPKCKNGGTCYTHFTG 483  
QY 434 --CEC-AGY-GGNCQFLLPEPPGPV-----DEEQFPWAVCAGLV-LLLLGCAAVVCVR-- 481  
Db 484 NVCQCPTGFMGTSCFVRVHDPT-PASHRADSSNTLTMVCLGLLTFLLGCGVFMVRGM 542  
QY 482 -----LKQKPECETETMNNLANCO-----REKDS-----IGATQIKNTNKKDF 520  
Db 543 RRGHFNEKGRVNDLEPKNNLIEKPHFKMNPDPYLREKSSSKQKLLQGSESEERSGRR 602  
QY 521 HDKK-----VRYPDYNLVLVKHKKCESEKALRKRPSVYSTSKDTKYQSVYV-SEK 570

Db	603	TDRKPDTKQCNPTSRYP	-----	:		:		:	
Qy	571	DECI-ATEV	578						
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Db	634	EQCIFATEV	642						

Search completed: November 29, 2004, 13:26:08  
Job time : 72.5872 secs